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OM protein - protein search, using sw model

Run on: December 29, 2005, 15:28:28 ; Search time 184 Seconds  
(without alignments)  
47.759 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTYEGVLLKGGKREBEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003s.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	8 ADS13770	Adsl3770 Human Ang
2	106	100.0	20	8 ADS13769	Adsl3769 Human Ang
3	106	100.0	26	8 ADS13805	Adsl3805 Ang-1 lin
4	106	100.0	235	6 AAE32344	Aae32344 Human ang
5	106	100.0	261	8 ADI23636	Adi23636 Human Ang
6	106	100.0	298	8 ADI23638	Adi23638 Yeast GCN
7	106	100.0	310	8 ADI23640	Adi23640 Human CMP
8	106	100.0	312	8 ADI23642	Adi23642 Human COM
9	106	100.0	402	7 AAE38503	Aae38503 Human ang
10	106	100.0	402	9 AEA81248	Aea81248 Human ang
11	106	100.0	456	8 ADS13776	Adsl3776 Mouse Ang
12	106	100.0	456	8 ADS13775	Adsl3775 Human Ang
13	106	100.0	494	2 AA475226	Aa475226 Amino aci
14	106	100.0	498	2 AAR94603	Aar94603 Human TIE
15	106	100.0	498	2 AA01409	Aa01409 Human TIE
16	106	100.0	498	2 AA47530	Aa47530 Amino aci
17	106	100.0	498	2 AA47528	Aa47528 Amino aci
18	106	100.0	498	3 AAY78905	Aay78905 Human ang
19	106	100.0	498	3 AAY78902	Aay78902 Human ang
20	106	100.0	498	3 AAB28391	Aab28391 Human ang
21	106	100.0	498	5 AAU77943	Aau77943 Amino aci
22	106	100.0	498	6 ABP58063	Abp58063 Human ang
23	106	100.0	498	6 AAE32342	Aae32342 Human ang
24	106	100.0	498	7 AAE38487	Aae38487 Mouse ang

25	106	100.0	498	7 AAE38507	Aae38507 Human ang
26	106	100.0	498	7 AAE38501	Aae38501 Human ang
27	106	100.0	498	7 AAE38499	Aae38499 Mouse ang
28	106	100.0	498	7 AAE38486	Aae38486 Human ang
29	106	100.0	498	7 AAE38497	Aae38497 Mouse ang
30	106	100.0	498	7 ADD69265	Add69265 Human ang
31	106	100.0	498	7 ADP72296	Adp72296 Human ang
32	106	100.0	498	8 ADQ19778	Adq19778 Human sof
33	106	100.0	498	8 ADR87238	Adr87238 Amino aci
34	106	100.0	498	8 ADS13782	Adsl3782 Mouse ang
35	106	100.0	498	8 ADS13781	Adsl3781 Human ang
36	106	100.0	498	9 ADZ80187	Adz80187 Human TIE
37	106	100.0	498	9 AEA81247	Aea81247 Human ang
38	106	100.0	498	9 AEB87759	Aeb87759 Human Ang
39	96	90.6	495	3 AAY78907	Aay78907 Angiopole
40	96	90.6	495	3 AAY78904	Aay78904 Angiopole
41	96	90.6	495	3 AAB28393	Aab28393 Human ang
42	96	90.6	495	5 AAU77945	Aau77945 Amino aci
43	96	90.6	498	7 AAE38493	Aae38493 Pig angio
44	93	87.7	27	8 ADS13806	Adsl3806 Ang-1 lin
45	89.5	84.4	147	7 AAE38508	Aae38508 Human ang

## ALIGNMENTS

RESULT 1  
ADSL3770  
ID ADS13770 standard; peptide; 20 AA.  
XX  
AC ADS13770;  
XX  
XX  
DT 02-DEC-2004 (first entry)  
XX  
XX  
DE Human Ang-1 protein ECM-binding fragment.  
XX  
XX  
KW Ang-1; extracellular matrix; ECM; angiotensin; vasotrophic;  
KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;  
KW gene therapy; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004076650-A2.  
XX  
PD 10-SEP-2004.  
XX  
PF 27-FEB-2004; 2004WO-US006101.  
XX  
PF 27-FEB-2003; 2003US-0450582P.  
PR (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Yu Q;  
XX  
XX  
DR WPI; 2004-653413/63.  
DR N-PSDB; ADS13788.  
XX  
PT New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischemia.  
PT  
PT  
PS Claim 1; SEQ ID NO 2; 114pp; English.  
XX  
XX  
CC The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases

CC related to lack of blood vessels such as ischaemia in hearts and limbs;  
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,  
 CC atherosclerosis risk by maintaining the health and integrity of blood  
 CC vessels; to assist the recovery of the patients who had stroke and the  
 CC angioplasty procedure by promoting the growth/survival of endothelial  
 CC cells and establish endothelial monolayer and inhibit excessive  
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;  
 CC to treat patients with restenosis by inhibiting re-closure of blood  
 CC vessel after inserting stents into blood vessels; to make stable and  
 CC functional artificial blood vessels comprising using the composition  
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;  
 CC of treating an individual suspected of having cancer; of preventing  
 CC diabetes and/or arthritis in an individual suspected of being at risk of  
 CC developing diabetes or arthritis. The pharmaceutical composition is  
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery  
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,  
 CC angiogenesis, or arthritis. The present sequence represents an ECM-  
 CC binding fragment of Ang-1 protein.  
 XX  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 106; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20  
 |||||  
 DB 1 LCTKEGVLLKGGKREBEKPF 20

## RESULT 2

ADSL3769  
 ID ADSL3769 standard; peptide; 20 AA.

XX AC ADSL3769;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Human Ang-1 protein ECM-binding fragment.  
 XX KW Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;  
 XX KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;  
 XX KW gene therapy; human.  
 XX OS Homo sapiens.  
 XX PN WO2004076650-A2.  
 XX PD 10-SEP-2004.  
 XX PF 27-FEB-2004; 2004WO-US006101.  
 XX PR 27-FEB-2003; 2003US-0450582P.  
 XX PA (UYPE-) UNIV PENNSYLVANIA.  
 XX PI Yu Q;  
 XX WPI; 2004-653413/63.  
 XX N-PSDB; ADSL3787.

XX New pharmaceutical composition comprises a pharmaceutical carrier and an  
 FT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein  
 FT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or  
 FT ischemia.

PS Claim 1; SEQ ID NO 1; 114pp; English.

XX The invention relates to a pharmaceutical composition comprising a  
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-  
 CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also  
 CC provided are methods of treating an individual suspected of having  
 CC coronary artery disease, vascular disease or a condition involving

CC ischaemia; of promoting angiogenesis, endothelial survival and  
 CC maintaining vascular integrity in an individual; of treating an  
 CC individual suspected of having a disease related to lack of blood vessels  
 CC to effectively promote angiogenesis in the patients with the diseases  
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;  
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,  
 CC atherosclerosis risk by maintaining the health and integrity of blood  
 CC vessels; to assist the recovery of the patients who had stroke and the  
 CC angioplasty procedure by promoting the growth/survival of endothelial  
 CC cells and establish endothelial monolayer and inhibit excessive  
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;  
 CC to treat patients with restenosis by inhibiting re-closure of blood  
 CC vessel after inserting stents into blood vessels; to make stable and  
 CC functional artificial blood vessels comprising using the composition  
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;  
 CC of treating an individual suspected of having cancer; of preventing  
 CC diabetes and/or arthritis in an individual suspected of being at risk of  
 CC developing diabetes or arthritis. The pharmaceutical composition is  
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery  
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,  
 CC angiogenesis, or arthritis. The present sequence represents an ECM-  
 CC binding fragment of Ang-1 protein.  
 XX

SQ Sequence 20 AA;

Query Match 100.0%; Score 106; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20  
 |||||  
 DB 1 LCTKEGVLLKGGKREBEKPF 20

## RESULT 3

ADSL3805  
 ID ADSL3805 standard; peptide; 26 AA.

XX AC ADSL3805;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Ang-1 linker peptide region.  
 XX KW Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;  
 XX KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;  
 XX KW gene therapy.  
 XX OS Homo sapiens.  
 XX PN WO2004076650-A2.  
 XX PD 10-SEP-2004.  
 XX PF 27-FEB-2004; 2004WO-US006101.  
 XX PR 27-FEB-2003; 2003US-0450582P.  
 XX PA (UYPE-) UNIV PENNSYLVANIA.  
 XX PI Yu Q;  
 XX WPI; 2004-653413/63.  
 XX New pharmaceutical composition comprises a pharmaceutical carrier and an  
 FT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein  
 FT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or  
 FT ischemia.  
 XX Example 1; Page 27; 114pp; English.  
 PS The invention relates to a pharmaceutical composition comprising a  
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-  
 CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also  
 CC provided are methods of treating an individual suspected of having  
 CC coronary artery disease, vascular disease or a condition involving

CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also  
 CC provided are methods of treating an individual suspected of having  
 CC coronary artery disease, vascular disease or a condition involving  
 CC ischaemia; of promoting angiogenesis, endothelial survival and  
 CC maintaining vascular integrity in an individual; of treating an  
 CC individual suspected of having a disease related to lack of blood vessels  
 CC to effectively promote angiogenesis in the patients with the diseases  
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;  
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,  
 CC atherosclerosis, risk by maintaining the health and integrity of blood  
 CC vessels; to assist the recovery of the patients who had stroke and the  
 CC angioplasty procedure by promoting the growth/survival of endothelial  
 CC cells and establish endothelial monolayer and inhibit excessive  
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;  
 CC to treat patients with restenosis by inhibiting re-closure of blood  
 CC vessel after inserting stents into blood vessels; to make stable and  
 CC functional artificial blood vessels comprising using the composition  
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;  
 CC of treating an individual suspected of having cancer; of preventing  
 CC diabetes and/or arthritis in an individual suspected of being at risk of  
 CC developing diabetes or arthritis. The pharmaceutical composition is  
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery  
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,  
 CC angiogenesis, or arthritis. The present sequence represents a linker  
 CC peptide region of Ang-1 protein.

XX SQ Sequence 26 AA;  
 Query Match 100.0%; Score 106; DB 8; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20  
 |||||  
 Db 7 LCTKEGVLKGGKREKEKPF 26

RESULT 4  
 ID AAE32344 standard; protein; 235 AA.  
 AC AAE32344;  
 DT 24-MAR-2003 (first entry)  
 DE Human angiotensin-1 (Ang-1) truncated protein #1.  
 KW Vascular endothelial growth factor; VEGF; angiogenesis; wound healing;  
 KW bone growth; osteoporosis; osteoarthritis; bone reconstruction; ulcer;  
 KW lesion; injury; trauma; periodontal condition; protein therapy; human;  
 KW angiotensin-1; Ang-1.

XX Homo sapiens.  
 XX WO200283851-A2.  
 XX 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US011406.  
 XX 10-APR-2001; 2001US-00832355.  
 XX (GENV-) GENVEC INC.  
 XX Kovesdi I, Kessler PD;  
 XX WPI; 2003-075536/07.  
 XX New fusion protein comprising a non-heparin-binding vascular endothelial  
 XX growth factor (VEGF) peptide portion and a non-VEGF peptide portion,  
 XX useful for promoting angiogenesis and/or bone growth in mammals.  
 XX Disclosure; Page 126-127; 191pp; English.

XX The invention relates to a fusion protein comprising non-heparin binding  
 CC vascular endothelial growth factor (VEGF) peptide portion and a non-VEGF  
 CC peptide portion useful for promoting angiogenesis and/or bone growth in  
 CC mammalian host. The fusion protein is useful for promoting angiogenesis,  
 CC wound healing and bone growth. Compositions containing bone growth  
 CC promoting fusion protein can be used to treat osteoporosis, rheumatoid or  
 CC osteoarthritis, to improve poor bone healing, to promote implant  
 CC integration and function of artificial joints and to facilitate bone  
 CC reconstruction. They can also be used to treat e.g. ulcers, lesions,  
 CC injuries, burns, trauma, periodontal conditions, lacerations and other  
 CC conditions. The invention is also useful in protein therapy. The present  
 CC sequence is human angiotensin-1 (Ang-1) truncated protein used in the  
 CC invention  
 XX SQ Sequence 235 AA;

Query Match 100.0%; Score 106; DB 6; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20  
 |||||  
 Db 215 LCTKEGVLKGGKREKEKPF 234

RESULT 5  
 ID ADI23636 standard; protein; 261 AA.  
 AC ADI23636;  
 DT 22-APR-2004 (first entry)  
 DE Human Ang-1 fibrinogen-like domain/Preprotrypsin signal.

XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;  
 KW angiotensin; coiled-coil domain; cell growth; proliferation;  
 KW matrix protein; transcription factor; growth factor; secretory protein;  
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;  
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;  
 KW endothelial precursor cell.

XX Homo sapiens.  
 OS Synthetic.  
 XX US2003220476-A1.  
 XX 27-NOV-2003.  
 XX 18-OCT-2002; 2002US-00273180.  
 XX 21-MAY-2002; 2002US-0382541P.  
 XX (KOHG/) KOH G Y.  
 XX Koh GY;  
 XX WPI; 2004-010889/01.  
 XX N-PSDB; ADI23635.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked  
 PT to either a receptor binding domain of ligand or ligand binding domain of  
 PT a receptor, useful for inhibiting or promoting differential function.  
 XX Disclosure; SEQ ID NO 2; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a  
 CC coiled-coil domain linked to either a receptor binding domain of a ligand  
 CC or ligand binding domain of a receptor, which forms a biologically active  
 CC multimer, and where the chimaeric molecule in its non-multimeric form is  
 CC not biologically active. Also included are an isolated nucleic acid  
 CC encoding the coiled coil chimaeric molecule, an expression vector

CC comprising the nucleic acid, a host cell comprising the vector, a soluble  
 CC biologically active multimer comprising the coiled coil chimaeric  
 CC molecule, promoting cell growth or proliferation, decreasing or  
 CC inhibiting ligand activity or cell proliferation and making a chimaeric  
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging  
 CC to a matrix protein family, transcription factor family, growth factor  
 CC family or secretory protein family. The coiled coil domain is from  
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein  
 CC (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The  
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -  
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or  
 CC inhibiting a differential function and/or influencing the phenotype, such  
 CC as growth, survival, contractility, migration and/or proliferation of  
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem  
 CC cells and endothelial precursor cells. The present sequence represents  
 CC the fibrinogen-like domain of Ang-1 with a preprotrypsin leader.

XX Sequence 261 AA;

Query Match 100.0%; Score 106; DB 8; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20  
 Db 139 LCTKEGVLLKGGKREBEKPF 158

RESULT 6  
 ADI23638  
 ID ADI23638 standard; protein; 298 AA.

XX AC ADI23638;

XX DT 22-APR-2004 (first entry)

XX DE Yeast GCN4 coiled-coil domain/Human Ang-1 cDNA.

XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;  
 KW angiopoietin1; coiled-coil domain; cell growth; proliferation;  
 KW matrix protein; transcription factor; growth factor; secretory protein;  
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;  
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;  
 KW endothelial precursor cell; yeast.

XX OS Homo sapiens.

OS Saccharomyces cerevisiae.

OS Chimeric.

XX US2003220476-A1.

XX PD 27-NOV-2003.

XX PF 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

XX PI Koh GY;

XX DR WPI; 2004-010889/01.

XX DR N-PSDB; ADI23637.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked  
 FT to either a receptor binding domain of ligand or ligand binding domain of  
 PT a receptor, useful for inhibiting or promoting differential function.

XX Example 5; SEQ ID NO 4; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a  
 CC coiled-coil domain linked to either a receptor binding domain of a ligand  
 CC or ligand binding domain of a receptor, which forms a biologically active

CC multimer, and where the chimaeric molecule in its non-multimeric form is  
 CC not biologically active. Also included are an isolated nucleic acid  
 CC encoding the coiled coil chimaeric molecule, an expression vector  
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble  
 CC biologically active multimer comprising the coiled coil chimaeric  
 CC molecule, promoting cell growth or proliferation, decreasing or  
 CC inhibiting ligand activity or cell proliferation and making a chimaeric  
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging  
 CC to a matrix protein family, transcription factor family, growth factor  
 CC family or secretory protein family. The coiled coil domain is from  
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein  
 CC (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The  
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -  
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or  
 CC inhibiting a differential function and/or influencing the phenotype, such  
 CC as growth, survival, contractility, migration and/or proliferation of  
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem  
 CC cells and endothelial precursor cells. The present sequence represents  
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-  
 CC coil domain.

XX Sequence 298 AA;

Query Match 100.0%; Score 106; DB 8; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20  
 Db 64 LCTKEGVLLKGGKREBEKPF 83

RESULT 7

ADI23640

ID ADI23640 standard; protein; 310 AA.

XX AC ADI23640;

XX DT 22-APR-2004 (first entry)

XX DE Human CMP coiled-coil domain/Ang-1.

XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;  
 KW angiopoietin1; coiled-coil domain; cell growth; proliferation;  
 KW matrix protein; transcription factor; growth factor; secretory protein;  
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;  
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;  
 KW endothelial precursor cell.

XX OS Homo sapiens.

OS Synthetic.

XX US2003220476-A1.

XX PD 27-NOV-2003.

XX PF 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

XX PI Koh GY;

XX DR WPI; 2004-010889/01.

XX DR N-PSDB; ADI23639.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked  
 FT to either a receptor binding domain of ligand or ligand binding domain of  
 PT a receptor, useful for inhibiting or promoting differential function.

XX Example 6; SEQ ID NO 6; 38pp; English.

CC The invention relates to a coiled coil chimaeric molecule comprising a  
 CC coiled-coil domain linked to either a receptor binding domain of a ligand  
 CC or ligand binding domain of a receptor, which forms a biologically active  
 CC multimer, and where the chimaeric molecule in its non-multimeric form is  
 CC not biologically active. Also included are an isolated nucleic acid  
 CC encoding the coiled coil chimaeric molecule, an expression vector  
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble  
 CC biologically active multimer comprising the coiled coil chimaeric  
 CC molecule, promoting cell growth or proliferation, decreasing or  
 CC inhibiting ligand activity or cell proliferation and making a chimaeric  
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging  
 CC to a matrix protein family, transcription factor family, growth factor  
 CC family or secretory protein family. The coiled coil domain is from  
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein  
 CC (COMP). The receptor-binding domain binds to Tie2 or Tiel receptor. The  
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -  
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or  
 CC inhibiting a differential function and/or influencing the phenotype of  
 CC as growth, survival, contractility, migration and/or proliferation of  
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem  
 CC cells and endothelial precursor cells. The present sequence represents  
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-  
 CC coil domain.  
 XX  
 SQ Sequence 310 AA;

Query Match 100.0%; Score 106; DB 8; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREBEKPF 20  
 |||||  
 Db 76 LCTKEGVLKGGKREBEKPF 95

RESULT 8  
 ADI23642  
 ID ADI23642 standard; protein; 312 AA.

XX AC ADI23642;  
 XX DT 22-APR-2004 (first entry)  
 XX XX Human COMP coiled-coil domain/Ang-1.

XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;  
 KW angiopoietin1; coiled-coil domain; cell growth; proliferation;  
 KW matrix protein; transcription factor; growth factor; secretory protein;  
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;  
 KW Tie2 receptor; Tiel receptor; endothelial cell; haematopoietic stem cell;  
 KW endothelial precursor cell.

XX Homo sapiens.  
 OS Synthetic.

XX US2003220476-A1.

XX 27-NOV-2003.

XX 18-OCT-2002; 2002US-00273180.

XX 21-MAY-2002; 2002US-0382541P.

XX (KOHG/) KOH G Y.

XX Koh GY;

XX WPI; 2004-010889/01.  
 DR N-PSDB; ADI23641.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked  
 PT to either a receptor binding domain of ligand or ligand binding domain of  
 PT a receptor, useful for inhibiting or promoting differential function.

XX Example 7; SEQ ID NO 8; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a  
 CC coiled-coil domain linked to either a receptor binding domain of a ligand  
 CC or ligand binding domain of a receptor, which forms a biologically active  
 CC multimer, and where the chimaeric molecule in its non-multimeric form is  
 CC not biologically active. Also included are an isolated nucleic acid  
 CC encoding the coiled coil chimaeric molecule, an expression vector  
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble  
 CC biologically active multimer comprising the coiled coil chimaeric  
 CC molecule, promoting cell growth or proliferation, decreasing or  
 CC inhibiting ligand activity or cell proliferation and making a chimaeric  
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging  
 CC to a matrix protein family, transcription factor family, growth factor  
 CC family or secretory protein family. The coiled coil domain is from  
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein  
 CC (COMP). The receptor-binding domain binds to Tie2 or Tiel receptor. The  
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -  
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or  
 CC inhibiting a differential function and/or influencing the phenotype, such  
 CC as growth, survival, contractility, migration and/or proliferation of  
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem  
 CC cells and endothelial precursor cells. The present sequence represents  
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-  
 CC coil domain.  
 XX

SQ Sequence 312 AA;

Query Match 100.0%; Score 106; DB 8; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREBEKPF 20  
 |||||  
 Db 78 LCTKEGVLKGGKREBEKPF 97

RESULT 9  
 AAE38503

ID AAE38503 standard; protein; 402 AA.

XX AC AAE38503;

XX DT 20-NOV-2003 (first entry)

XX Human angiopoietin-1 #4.

XX Angiopoietin-1; endothelium; cell proliferation; tumour; gene therapy;  
 KW human.

XX Homo sapiens.

XX WO2003068165-A2.

XX 21-AUG-2003.

XX 14-FEB-2003; 2003WO-US004595.

XX 14-FEB-2002; 2002US-0356809P.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Ellis LM;

XX WPI; 2003-697465/66.

XX Stabilizing the endothelium or reducing endothelial cell proliferation  
 PT associated with a tumor comprises administering to a patient having a  
 PT tumor angiopoietin-1 polypeptide.

XX Disclosure; Page 139-140; 157pp; English.

CC The invention relates to a method for stabilising the endothelium or  
 CC reducing endothelial cell proliferation associated with a tumour by  
 CC administering angiotensin-1 peptide to a patient having tumour. The  
 CC method is useful for stabilising the endothelium or reducing endothelial  
 CC cell proliferation associated with a tumour. It is also useful in gene  
 CC therapy. The present sequence is human angiotensin-1. This sequence is  
 CC used to illustrate the method of the invention  
 XX  
 SQ Sequence 402 AA;

Query Match 100.0%; Score 106; DB 7; Length 402;  
 Best Local Similarity 100.0%; Pred. NO. 2.2e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20  
 DB 264 LCTKEGVLLKGGKREBEKPF 283

RESULT 10  
 AEA81248  
 ID AEA81248 standard; protein; 402 AA.

XX AEA81248;  
 XX  
 XX 25-AUG-2005 (first entry)

XX Human angiotensin 1 (ANGPT1), transcript variant 2 protein.

XX screening; obesity; nutritional disorder; anorectic; angiotensin 1;  
 XX ANGPT1; transcript variant.

XX Homo sapiens.

XX US2005136465-A1.

XX 23-JUN-2005.

XX 22-DEC-2004; 2004US-00019829.

XX 22-DEC-2003; 2003EP-00104902.

XX (CLERC/) CLERC R G.  
 XX (DUCH/) DUCHATEAU-NGUYEN G.  
 XX (GARD/) GARDES C.  
 XX (MIZR/) MIZRAHI J.  
 XX (OSTE/) OSTENSON C.

XX Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;  
 XX WPI; 2005-457507/46.  
 XX N-PSDB; AEA81187.

XX Screening test compounds that reduce and/or prevent obesity involves  
 XX contacting cell expressing gene from alpha-two-glycoprotein.

XX Claim 20; SEQ ID NO 115; 21pp; English.

XX The invention relates to a novel method for screening for test compounds  
 CC that reduce and/or prevent obesity. The method comprises contacting a  
 CC cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a  
 CC compound. The method of the invention demonstrates anorectic applications  
 CC and may be useful for screening for compounds that reduce and/or prevent  
 CC obesity. The current sequence is that of the human angiotensin 1  
 CC (ANGPT1), transcript variant 2 protein of the invention. The sequence  
 CC listing for the specification can be located via the USPTO web-site.

XX Sequence 402 AA;

Query Match 100.0%; Score 106; DB 9; Length 402;  
 Best Local Similarity 100.0%; Pred. NO. 2.2e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20  
 DB 264 LCTKEGVLLKGGKREBEKPF 283

RESULT 11  
 ADS13776

ID ADS13776 standard; protein; 456 AA.

XX ADS13776;

XX 02-DEC-2004 (first entry)

XX Mouse Ang-1 protein non-ECM-binding fragment.

XX Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;  
 XX antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;  
 XX gene therapy; mouse.

XX Mus sp.

XX WC004076650-A2.

XX 10-SEP-2004.

XX 27-FEB-2004; 2004WO-US006101.

XX 27-FEB-2003; 2003US-0450582P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

XX N-PSDB; ADS13794.

XX New pharmaceutical composition comprises a pharmaceutical carrier and an  
 amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein  
 or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or  
 ischemia.

XX Claim 5; SEQ ID NO 8; 114pp; English.

XX The invention relates to a pharmaceutical composition comprising a  
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-  
 CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also  
 CC provided are methods of treating an individual suspected of having  
 CC coronary artery disease, vascular disease or a condition involving  
 CC ischaemia; of promoting angiogenesis, endothelial survival and  
 CC maintaining vascular integrity in an individual; of treating an  
 CC individual suspected of having a disease related to lack of blood vessels  
 CC to effectively promote angiogenesis in the patients with the diseases  
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;  
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,  
 CC atherosclerosis risk by maintaining the health and integrity of blood  
 CC vessels; to assist the recovery of the patients who had stroke and the  
 CC angioplasty procedure by promoting the growth/survival of endothelial  
 CC cells and establish endothelial monolayer and inhibit excessive  
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;  
 CC to treat patients with restenosis by inhibiting re-closure of blood  
 CC vessel after inserting stents into blood vessels; to make stable and  
 CC functional artificial blood vessels comprising using the composition  
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;  
 CC of treating an individual suspected of having cancer; of preventing  
 CC diabetes and/or arthritis in an individual suspected of being at risk of  
 CC developing diabetes or arthritis. The pharmaceutical composition is  
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery  
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,  
 CC angiogenesis, or arthritis. The present sequence represents a non-ECM-  
 CC binding fragment of Ang-1 protein.

XX Sequence 456 AA;

Query Match 100.0%; Score 106; DB 8; Length 456;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREEEKPF 20  
 |||||  
 DB 222 LCTKEGVLKGGKREEEKPF 241

RESULT 12  
 ADS13775  
 ID ADS13775 standard; protein; 456 AA.  
 XX  
 AC ADS13775;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human Ang-1 protein non-ECM-binding fragment.  
 XX  
 KW Ang-1; extracellular matrix; ECM; angiotensin; cytotatic; vasotropic;  
 KW antidiabetic; antiarthritic; cerebroprotective; angiogenic;  
 KW gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02004076650-A2.  
 XX  
 PD 10-SEP-2004.  
 XX  
 PF 27-FEB-2004; 2004WO-US006101.  
 XX  
 PR 27-FEB-2003; 2003US-0450582P.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Yu Q;  
 XX  
 DR WPI; 2004-653413/63.  
 DR N-PSDB; ADS13793.  
 XX  
 PT New pharmaceutical composition comprises a pharmaceutical carrier and an  
 PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein  
 PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or  
 PT ischemia.  
 XX  
 PS Claim 5; SEQ ID NO 7; 114pp; English.  
 XX  
 CC The invention relates to a pharmaceutical composition comprising a  
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-  
 CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also  
 CC provided are methods of treating an individual suspected of having  
 CC coronary artery disease, vascular disease or a condition involving  
 CC ischaemia; of promoting angiogenesis, endothelial survival and  
 CC maintaining vascular integrity in an individual; of treating an  
 CC individual suspected of having a disease related to lack of blood vessels  
 CC to effectively promote angiogenesis in the patients with the diseases  
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;  
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,  
 CC atherosclerosis risk by maintaining the health and integrity of blood  
 CC vessels; to assist the recovery of the patients who had stroke and the  
 CC angioplasty procedure by promoting the growth/survival of endothelial  
 CC cells and establish endothelial monolayer and inhibit excessive  
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;  
 CC to treat patients with restenosis by inhibiting re-closure of blood  
 CC vessel after inserting stents into blood vessels; to make stable and  
 CC functional artificial blood vessels comprising using the composition  
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;  
 CC of treating an individual suspected of having cancer; of preventing  
 CC diabetes and/or arthritis in an individual suspected of being at risk of  
 CC developing diabetes or arthritis. The pharmaceutical composition is  
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery  
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,  
 CC angiogenesis, or arthritis. The present sequence represents a non-ECM-

CC binding fragment of Ang-1 protein.  
 XX  
 SQ Sequence 456 AA;  
 Query Match 100.0%; Score 106; DB 8; Length 456;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREEEKPF 20  
 |||||  
 DB 222 LCTKEGVLKGGKREEEKPF 241

RESULT 13  
 AAW47526  
 ID AAW47526 standard; protein; 494 AA.  
 XX  
 AC AAW47526;  
 XX  
 DT 09-SEP-1998 (first entry)  
 XX  
 DE Amino acid sequence of chimeric TIE ligand 2N1C1F (chimera 4).  
 XX  
 KW Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation; tumour;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09805779-A1.  
 XX  
 PD 12-FEB-1998.  
 XX  
 PF 01-AUG-1997; 97WO-US013557.  
 XX  
 PR 02-AUG-1996; 96US-0022999P.  
 PR 25-OCT-1996; 96US-00740223.  
 XX  
 PA (REGE-) REGENERON PHARM INC.  
 XX  
 PI Davis S, Yancopoulos GD;  
 DR WPI; 1998-145615/13.  
 DR N-PSDB; AAV18613.  
 XX  
 PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound  
 PT healing.  
 XX  
 PS Claim 20; Fig 27; 202pp; English.  
 XX  
 CC This is the amino acid sequence of the chimeric TIE ligand 2N1C1F, used  
 CC in the method of the invention, involving the production of TIE-2 ligands  
 CC which promote healing. The nucleic acids, vectors and host cells used in  
 CC the method of the invention are useful for the recombinant production of  
 CC the ligands. The ligands, etc. are useful for blocking blood vessel  
 CC growth, promoting neovascularisation, promoting the growth or  
 CC differentiation of a cell expressing the TIE receptor, blocking the  
 CC growth or differentiation of a cell expressing the TIE receptor and for  
 CC attenuating or preventing tumour growth in a human  
 XX  
 SQ Sequence 494 AA;  
 Query Match 100.0%; Score 106; DB 2; Length 494;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREEEKPF 20  
 |||||  
 DB 260 LCTKEGVLKGGKREEEKPF 279

RESULT 14  
 AAR94603  
 ID AAR94603 standard; protein; 498 AA.



```

XX AAR94603;
AC
XX 28-OCT-1996 (first entry)
DT
XX Human TIE-2 ligand 1 derived from lambda-gt10 clone.
XX
XX Angiogenesis; neovascularisation; tumour development; wound healing; TIE;
XX tyrosine kinase with Ig and EGF homology domains; vector; recombinant;
XX clone; diagnosis; ischaemia; thromboembolytic disease; atherosclerosis;
XX inflammation; diabetes; ligand bodies; delivery; targeting.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 269
XX /note= "extra Gly residue not present in TIE-2 ligand 1
XX derived from T98G clone (see AAT14649 and AAR94604)"
XX
XX WO9611269-A2.
XX
XX 18-APR-1996.
XX
XX 06-OCT-1995; 95WO-US012935.
XX
XX 07-OCT-1994; 94US-00319932.
XX
XX 27-OCT-1994; 94US-00330261.
XX
XX 02-DEC-1994; 94US-00348492.
XX
XX 09-DEC-1994; 94US-00353503.
XX
XX 17-JAN-1995; 95US-00373579.
XX
XX 06-APR-1995; 95US-00418595.
XX
XX (REGE-) REGENERON PHARM INC.
XX
XX Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisompierre PC;
XX Radziejewski C, Jones PF, Yancopoulos GD;
XX WPI; 1996-209850/21.
XX N-PSDB; AAT14648.
XX
XX Nucleic acid encoding TIE-2 ligand and related vectors - useful in
XX diagnosis and treatment of neovascularisation, tumours, etc., or to
XX promote wound healing, etc.
XX
XX Claim 2; Fig 4; 84pp; English.
XX
XX AAR94603 is a recombinant human TIE-2 (HTIE-2) ligand 1 derived from a
XX lambda-gt10 clone. The ligand has an extra Gly residue (aa 269) as
XX compared to the hTIE-2 ligand from a T98G clone (see AAT14649 and
XX AAR94604). hTIE-2 ligand DNAs of the invention are recombinant versions
XX of the native ligand coding sequences and may be used to produce the
XX ligands at a high yield. Antibodies and receptor bodies that bind to TIE-
XX 2 ligands may be used to inhibit angiogenesis and neovascularisation
XX (e.g. associated with tumour development) and the TIE-2 ligands
XX themselves are useful to promote neovascularisation and wound healing
XX e.g. for treatment of ischaemia. TIE-2 ligands are also useful to treat
XX thromboembolytic disease, atherosclerosis, inflammation and diabetes.
XX Ligand bodies contg. TIE-2 ligands may also be useful for the delivery
XX and targeting of growth factors, toxins etc. to sites where their
XX presence is advantageous
XX
XX Sequence 498 AA;
SQ
Query Match 100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LCTKEGVLLKGGKREEEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 264 LCTKEGVLLKGGKREEEKPF 283

RESULT 15

```

```

AAW01409
ID AAW01409 standard; protein; 498 AA.
XX
XX AAW01409;
AC
XX 11-FEB-1997 (first entry)
DT
XX Human TIE-2 ligand 1 (lambda-gt10 clone product).
XX
XX TIE-2 ligand 1; tyrosine kinase with Ig and EGF homology domain;
XX receptor; agonist; neovascularisation; wound healing; ischaemia;
XX leukaemia; thrombocytopaenia; anaemia; angiogenesis; tumour;
XX atherosclerosis; inflammation; diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 269
XX /note= "Gly-269 is absent in TIE-2 ligand 1 from
XX glioblastoma T98G"
XX
XX WO9631598-A1.
XX
XX 10-OCT-1996.
XX
XX 05-APR-1996; 96WO-US004806.
XX
XX 06-APR-1995; 95US-00418595.
XX
XX 06-OCT-1995; 95WO-US012935.
XX
XX (REGE-) REGENERON PHARM INC.
XX
XX Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisompierre PC;
XX Radziejewski C, Jones PF, Yancopoulos GD;
XX WPI; 1996-465021/46.
XX N-PSDB; AAT44319.
XX
XX TIE-2 agonists and antagonists and related DNA - useful for promoting or
XX blocking neovascularisation, etc.
XX
XX Claim 14; Fig 4; 113pp; English.
XX
XX Human TIE-2 (tyrosine kinase with Ig and EGF homology domains) ligand 1
XX (AAW01409) is a ligand that binds the TIE-2 receptor. Its amino acid
XX sequence was deduced from a cDNA clone (AAT44319) derived from foetal
XX lung cells. A variant form of the ligand (AAW01410), lacking Gly-269, is
XX produced by a cDNA clone (AAT44320) from glioblastoma T98G cells. Both
XX ligands are TIE-2 agonists useful in promoting the growth, survival,
XX migration and/or differentiation and/or stabilisation or destabilisation
XX of cells expressing the TIE-2 receptor. They can be isolated from natural
XX sources or produced in transformed host cells
XX
XX Sequence 498 AA;
SQ
Query Match 100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LCTKEGVLLKGGKREEEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 264 LCTKEGVLLKGGKREEEKPF 283

Search completed: December 29, 2005, 15:36:17
Job time : 186 secs

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OM protein - protein search, using sw model

Run on: December 29, 2005, 15:32:59 ; Search time 46 Seconds  
(without alignments)  
35.946 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKRGVLLKGRKEEKPF 20

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/PCUTUS\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	478	2	US-08-740-223A-7
2	106	100.0	478	2	US-09-709-188-7
3	106	100.0	478	2	US-10-225-060-7
4	106	100.0	495	2	US-08-740-223A-26
5	106	100.0	495	2	US-09-709-188-26
6	106	100.0	495	2	US-10-225-060-26
7	106	100.0	497	2	US-08-740-223A-14
8	106	100.0	497	2	US-09-709-188-14
9	106	100.0	497	2	US-10-225-060-14
10	106	100.0	498	1	US-08-373-579-2
11	106	100.0	498	1	US-08-418-595-2
12	106	100.0	498	1	US-08-665-926-2
13	106	100.0	498	1	US-08-348-452-2
14	106	100.0	498	2	US-09-162-437-2
15	106	100.0	498	2	US-08-740-223A-2
16	106	100.0	498	2	US-08-740-223A-20
17	106	100.0	498	2	US-09-351-457-2
18	106	100.0	498	2	US-09-561-500-2
19	106	100.0	498	2	US-09-561-108-2
20	106	100.0	498	2	US-09-351-543-2
21	106	100.0	498	2	US-09-561-526-2
22	106	100.0	498	2	US-09-202-491-5
23	106	100.0	498	2	US-09-202-491-6
24	106	100.0	498	2	US-08-817-318-2
25	106	100.0	498	2	US-09-709-188-2
26	106	100.0	498	2	US-09-709-188-20
27	106	100.0	498	2	US-09-561-499-2

Sequence 2, Appli  
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Sequence 5, Appli  
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ALIGNMENTS

RESULT 1  
US-08-740-223A-7  
; Sequence 7, Application US/08740223A  
; Patent No. 6265564  
; GENERAL INFORMATION:  
; APPLICANT: Davis, et al.  
; TITLE OF INVENTION: Expressed Ligand - Vascular  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill Road  
; CITY: Tarrytown  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/740, 223A  
; FILING DATE: 25-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 60/022/999  
; FILING DATE: 02-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cobert, Robert J  
; REGISTRATION NUMBER: 36,108  
; REFERENCE/DOCKET NUMBER: REG 333  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 914-345-7400  
; TELEFAX: 914-345-7721  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 478 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Mature T11 protein  
; LOCATION: 1...478  
; OTHER INFORMATION:  
; US-08-740-223A-7

Query Match 100.0%; Score 106; DB 2; Length 478;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGGKREERKPF 20
    |||||
Db 244 LCTKEGVLLKGGKREERKPF 263

RESULT 2
US-09-709-188-7
; Sequence 7, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-188-7

Query Match 100.0%; Score 106; DB 2; Length 478;
-Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGGKREERKPF 20
    |||||
Db 244 LCTKEGVLLKGGKREERKPF 263

RESULT 3
US-10-225-060-7
; Sequence 7, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7

Query Match 100.0%; Score 106; DB 2; Length 478;
-Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGGKREERKPF 20
    |||||
Db 244 LCTKEGVLLKGGKREERKPF 263

RESULT 4
US-08-740-223A-26
; Sequence 26, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
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; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; TITLE OF INVENTION: Intercellular Signaling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: 2N1C1P (chimera 4)
; LOCATION: 1...495
; OTHER INFORMATION:
US-08-740-223A-26

Query Match 100.0%; Score 106; DB 2; Length 495;
-Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGGKREERKPF 20
    |||||
Db 261 LCTKEGVLLKGGKREERKPF 280

RESULT 5
US-09-709-188-26
; Sequence 26, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
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; Sequence 2, Application US/08665926
; Patent No. 5851797
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al.
; TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,926
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert J. Cobert
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-2113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-926-2

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREEEKPF 20
Db 264 LCTKEGVLKGGKREEEKPF 283

RESULT 13
US-08-348-492-2
; Sequence 2, Application US/08348492
; Patent No. 5879672
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,492
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempner, Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 330B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 347-7000
; TELEFAX: (914) 347-2113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-348-492-2

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREEEKPF 20
Db 264 LCTKEGVLKGGKREEEKPF 283

RESULT 14
US-09-162-437-2
; Sequence 2, Application US/09162437
; Patent No. 6166185
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/162,437
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/418,595
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
; FILING DATE: 17-JAN-1995
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.

```

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/ / REGISTRATION NUMBER: 36,108
/ / REFERENCE/DOCKET NUMBER: REG 330-D
/ / TELECOMMUNICATION INFORMATION:
/ / TELEPHONE: (914) 345-7400
/ / TELEFAX: (914) 345-7721
/ / INFORMATION FOR SEQ ID NO: 2:
/ / SEQUENCE CHARACTERISTICS:
/ / LENGTH: 498 amino acids
/ / TYPE: amino acid
/ / TOPOLOGY: linear
/ / MOLECULE TYPE: protein
/ / US-09-162-437-2

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Query Match      100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20: Conservative 0; Mismatches 0; Indels
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Qy 1 LCTKEGVLLKGGKREEKPF 20  
264 LCTKEGVLLKGGKREEKPF 283

## RESULT 15

US-08/740-223A-2  
Sequence 2, Application US/08740223A  
Patent No. 6265564  
GENERAL INFORMATION:  
APPLICANT: Davis, et al.  
TITLE OF INVENTION: Expressed Ligand  
TITLE OF INVENTION: Intercellular Si  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals  
STREET: 777 Old Saw Mill Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSQL Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/740,223A  
FILING DATE: 25-OCT-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US95 60/022/999  
FILING DATE: 02-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Cobert, Robert J  
REGISTRATION NUMBER: 36,108  
REFERENCE/DOCKET NUMBER: REG 333  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 498 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Human TIE-2 ligand 1  
LOCATION: 1...498  
OTHER INFORMATION: from clone gtl1  
OTHER INFORMATION: ligand 1  
US-08/740-223A-2

Query Match 100.0%; Score 106; DB 2; Length 498;

Best Local Similarity	100.0%	Pred. No.	3.3e-09;
Matches	20;	Conservative	0;
Mismatches	0;	Indels	0;
Gaps	0;	Gaps	0;

QY 1 LCTKEGVLKGGKREEKPF 20  
|||  
Db 264 LCTKEGVLKGGKREEKPF 283

Search completed: December 29, 2005, 15:41:47  
Job time : 47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 15:36:24 ; Search time 160 Seconds  
(without alignments)  
52.229 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREEEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	4	US-10-789-222-1
2	106	100.0	20	4	US-10-789-222-2
3	106	100.0	235	3	US-09-832-355A-18
4	106	100.0	260	4	US-10-273-180-2
5	106	100.0	298	4	US-10-273-180-4
6	106	100.0	309	4	US-10-273-180-6
7	106	100.0	312	4	US-10-273-180-8
8	106	100.0	402	4	US-10-367-259A-36
9	106	100.0	402	6	US-11-019-829-115
10	106	100.0	456	4	US-10-789-222-7
11	106	100.0	456	4	US-10-789-222-8
12	106	100.0	478	4	US-10-225-060-7
13	106	100.0	478	5	US-10-928-911-7
14	106	100.0	478	6	US-11-073-120-7
15	106	100.0	495	4	US-10-225-060-26
16	106	100.0	495	5	US-10-928-911-26
17	106	100.0	495	6	US-11-073-120-26
18	106	100.0	497	4	US-10-225-060-14
19	106	100.0	497	5	US-10-928-911-14
20	106	100.0	497	6	US-11-073-120-14
21	106	100.0	498	3	US-09-998-831-2
22	106	100.0	498	3	US-09-897-306-13
23	106	100.0	498	3	US-09-832-355A-15
24	106	100.0	498	3	US-09-998-833-2
25	106	100.0	498	4	US-10-179-744-2
26	106	100.0	498	4	US-10-186-817-2
27	106	100.0	498	4	US-10-215-224-5

Sequence 6, Appli  
Sequence 5, Appli  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 20, Appli  
Sequence 2, Appli  
Sequence 12, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 13, Appli  
Sequence 14, Appli  
Sequence 24, Appli  
Sequence 26, Appli  
Sequence 28, Appli  
Sequence 40, Appli  
Sequence 13, Appli  
Sequence 14, Appli

ALIGNMENTS

RESULT 1

US-10-789-222-1  
; Sequence 1, Application US/10789222  
; Publication No. US20040186054A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Qin  
; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses  
; TITLE OF INVENTION: of the Same  
; FILE REFERENCE: UPN0003-100 (P3115)  
; CURRENT APPLICATION NUMBER: US/10/789,222  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US 60/450,582  
; PRIOR FILING DATE: 2003-02-27  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-789-222-1

Query Match 100.0%; Score 106; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREEEKPF 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 LCTKEGVLLKGGKREEEKPF 20

RESULT 2

US-10-789-222-2  
; Sequence 2, Application US/10789222  
; Publication No. US20040186054A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Qin  
; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses  
; TITLE OF INVENTION: of the Same  
; FILE REFERENCE: UPN0003-100 (P3115)  
; CURRENT APPLICATION NUMBER: US/10/789,222  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US 60/450,582  
; PRIOR FILING DATE: 2003-02-27  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: mouse  
US-10-789-222-2

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Query Match      100.0%; Score 106; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREEEKPF 20
Db      1 LCTKEGVLLKGGKREEEKPF 20
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RESULT 3
US-09-832-355A-18
; Sequence 18, Application US/09832355A
; Publication No. US20030027751A1
; GENERAL INFORMATION:
; APPLICANT: Kovesdi, Imre
; APPLICANT: Kessler, Paul
; TITLE OF INVENTION: VEGF FUSION PROTEINS
; FILE REFERENCE: 205654
; CURRENT APPLICATION NUMBER: US/09/832.355A
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-355A-18

Query Match      100.0%; Score 106; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREEEKPF 20
Db     215 LCTKEGVLLKGGKREEEKPF 234
|||||
|||||

RESULT 4
US-10-273-180-2
; Sequence 2, Application US/10273180
; Publication No. US20030220476A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/10/273.180
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-273-180-2

Query Match      100.0%; Score 106; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREEEKPF 20
Db     27 LCTKEGVLLKGGKREEEKPF 46
|||||
|||||

RESULT 5
US-10-273-180-4
; Sequence 4, Application US/10273180
; Publication No. US20030220476A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
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; CURRENT APPLICATION NUMBER: US/10/273.180
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-273-180-4

Query Match      100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREEEKPF 20
Db     64 LCTKEGVLLKGGKREEEKPF 83
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RESULT 6
US-10-273-180-6
; Sequence 6, Application US/10273180
; Publication No. US20030220476A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/10/273.180
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-273-180-6

Query Match      100.0%; Score 106; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREEEKPF 20
Db     75 LCTKEGVLLKGGKREEEKPF 94
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|||||

RESULT 7
US-10-273-180-8
; Sequence 8, Application US/10273180
; Publication No. US20030220476A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/10/273.180
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-273-180-8

Query Match      100.0%; Score 106; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREEEKPF 20
Db     78 LCTKEGVLLKGGKREEEKPF 97
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RESULT 8
US-10-367-259A-36
; Sequence 36, Application US/10367259A
; Publication No. US20030220250A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, LEE M.
; TITLE OF INVENTION: ANGIOPOIETIN-1 IN THE TREATMENT OF DISEASE
; FILE REFERENCE: UTSC:6980S
; CURRENT APPLICATION NUMBER: US/10/367,259A
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,809
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-259A-36

Query Match      100.0%; Score 106; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREBEKPF 20
Db      264 LCTKEGVLLKGGKREBEKPF 283

RESULT 9
US-11-019-829-115
; Sequence 115, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: angiotensin 1 variant 2
; LOCATION: (1)...(402)
; OTHER INFORMATION: LocusID: 284; NM_139290
US-11-019-829-115

Query Match      100.0%; Score 106; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREBEKPF 20
Db      264 LCTKEGVLLKGGKREBEKPF 283

RESULT 10
US-10-789-222-7
; Sequence 7, Application US/10789222
; Publication No. US20040186054A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: of the Same
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/450,582
; PRIOR FILING DATE: 2003-02-27

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; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-222-7

Query Match      100.0%; Score 106; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREBEKPF 20
Db      222 LCTKEGVLLKGGKREBEKPF 241

RESULT 11
US-10-789-222-8
; Sequence 8, Application US/10789222
; Publication No. US20040186054A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiotensin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,582
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 456
; TYPE: PRT
; ORGANISM: mouse
US-10-789-222-8

Query Match      100.0%; Score 106; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LCTKEGVLLKGGKREBEKPF 20
Db      222 LCTKEGVLLKGGKREBEKPF 241

RESULT 12
US-10-225-060-7
; Sequence 7, Application US/10225060
; Publication No. US20030092891A1
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7

Query Match      100.0%; Score 106; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LCTKEGVLLKGGKREEKPF 20  
|||  
Db 244 LCTKEGVLLKGGKREEKPF 263

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2005, 15:33:14 ; Search time 13 Seconds  
(without alignments)  
11.521 Million cell updates/sec

Title: US-10-789-222-1  
Perfect score: 106  
Sequence: 1 LCTKEGVLLKGGKREKPEF 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
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2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	44	41.5	275	7	US-11-110-977-2
2	43	40.6	415	7	US-11-182-946-6
3	43	40.6	589	6	US-10-467-657-4826
4	42.5	40.1	163	6	US-10-793-626-2598
5	41	38.7	134	6	US-10-467-657-7860
6	41	38.7	394	6	US-10-467-657-7966
7	41	38.7	412	7	US-11-082-389-96
8	40	37.7	257	6	US-10-632-150-40
9	40	37.7	257	7	US-11-073-457-40
10	40	37.7	257	7	US-11-073-460-40
11	39	36.8	70	7	US-11-057-047-3
12	39	36.8	245	6	US-10-131-826A-280
13	39	36.8	739	7	US-11-057-047-2
14	39	36.8	761	7	US-11-057-047-6
15	39	36.8	764	7	US-11-057-047-1
16	39	36.8	798	6	US-10-821-234-1034
17	38	35.8	213	6	US-10-995-561-842
18	38	35.8	213	6	US-10-995-561-843
19	38	35.8	213	6	US-10-995-561-845
20	38	35.8	247	6	US-10-131-826A-284
21	38	35.8	483	6	US-10-467-657-2774
22	38	35.8	598	7	US-11-082-389-398
23	38	35.8	739	7	US-11-107-028-6
24	38	35.8	968	7	US-11-000-463-281
25	37	34.9	145	6	US-10-467-657-6506

ALIGNMENTS

RESULT 1  
US-11-110-977-2  
; Sequence 2, Application US/11110977  
; Publication No. US20050260682A1  
; GENERAL INFORMATION:  
; APPLICANT: Charmley, Patrick R.  
; APPLICANT: Smith, Ryan C.  
; APPLICANT: Argonza-Barrett, Rhodora H.  
; APPLICANT: Fitzgibbon, Matthew P.  
; APPLICANT: Wang, Kai P.  
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis  
; FILE REFERENCE: CECH118764  
; CURRENT APPLICATION NUMBER: US/11/110,977  
; CURRENT FILING DATE: 2005-04-19  
; PRIOR APPLICATION NUMBER: US/10/112,645  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 60/280,514  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-11-110-977-2  
Query Match 41.5%; Score 44; DB 7; Length 275;  
Best Local Similarity 52.9%; Pred. No. 4.1;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 LCTKEGVLLKGGKREEE 17  
||: ||||: |||:  
Db 254 LCSSEVGLLNAREQE 270  
RESULT 2  
US-11-182-946-6  
; Sequence 6, Application US/11182946  
; Publication No. US20050255100A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.1280004  
; CURRENT APPLICATION NUMBER: US/11/182,946  
; CURRENT FILING DATE: 2005-07-18

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, PRIOR APPLICATION NUMBER: US/10/186,643
, PRIOR FILING DATE: 2002-07-02
, PRIOR APPLICATION NUMBER: US/09/573,986
, PRIOR FILING DATE: 2000-05-18
, NUMBER OF SEQ ID NOS: 27
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 6
, LENGTH: 415
, TYPE: PR1
, ORGANISM: Homo sapiens
US-11-182-946-6

Query Match      40.6%; Score 43; DB 7; Length 415;
Best Local Similarity 52.6%; Pred. No. 9.1;
Matches 10; Conservative 0; Mismatches 9; Indels 9; Gaps 0;

Qy 1 LCTKEGVLKGGKREBEK 19
Db 250 LCRKLGTLKRRHPGESSP 268

RESULT 3
US-10-467-657-4826
, Sequence 4826, Application US/10/467657
, Publication No. US20050260581A1
, GENERAL INFORMATION:
, APPLICANT: CHIRON Spa
, APPLICANT: FONTANA Maria Rita
, APPLICANT: PIZZA Mariagrazia
, APPLICANT: MASIGNANI Vega
, APPLICANT: MONACI Elisabetta
, TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
, FILE REFERENCE:
, CURRENT APPLICATION NUMBER: US/10/467,657
, CURRENT FILING DATE: 2003-08-11
, PRIOR APPLICATION NUMBER: GB-0103424.8
, PRIOR FILING DATE: 2001-02-12
, NUMBER OF SEQ ID NOS: 9218
, SOFTWARE: SeqWin99, version 1.04
, SEQ ID NO 4826
, LENGTH: 589
, TYPE: PR1
, ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4826

Query Match      40.6%; Score 43; DB 6; Length 589;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

Qy 6 GVLLKGGKREBEK 18
Db 365 GVSLAGAKQSEBK 377

RESULT 4
US-10-793-626-2598
, Sequence 2598, Application US/10/793626
, Publication No. US20050255478A1
, GENERAL INFORMATION:
, APPLICANT: KIMMERLY, WILLIAM JOHN
, TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
, FILE REFERENCE: PU3480US
, CURRENT APPLICATION NUMBER: US/10/793,626
, CURRENT FILING DATE: 2004-03-04
, PRIOR APPLICATION NUMBER: 60/164,258
, PRIOR FILING DATE: 1999-11-09
, NUMBER OF SEQ ID NOS: 4472
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 2598
, LENGTH: 163
, TYPE: PR1
, ORGANISM: Artificial Sequence
, FEATURE:

, PRIOR APPLICATION NUMBER: US/10/186,643
, PRIOR FILING DATE: 2002-07-02
, PRIOR APPLICATION NUMBER: US/09/573,986
, PRIOR FILING DATE: 2000-05-18
, NUMBER OF SEQ ID NOS: 27
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 6
, LENGTH: 415
, TYPE: PR1
, ORGANISM: Homo sapiens
US-11-182-946-6

Query Match      40.1%; Score 42.5; DB 6; Length 163;
Best Local Similarity 47.6%; Pred. No. 4.1;
Matches 10; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

Qy 1 LCTKEGVLKGGKREBEK 18
Db 142 ICTKEDIKAKVGRSREAPK 162

RESULT 5
US-10-467-657-7860
, Sequence 7860, Application US/10/467657
, Publication No. US20050260581A1
, GENERAL INFORMATION:
, APPLICANT: CHIRON Spa
, APPLICANT: FONTANA Maria Rita
, APPLICANT: PIZZA Mariagrazia
, APPLICANT: MASIGNANI Vega
, APPLICANT: MONACI Elisabetta
, TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
, FILE REFERENCE:
, CURRENT APPLICATION NUMBER: US/10/467,657
, CURRENT FILING DATE: 2003-08-11
, PRIOR APPLICATION NUMBER: GB-0103424.8
, PRIOR FILING DATE: 2001-02-12
, NUMBER OF SEQ ID NOS: 9218
, SOFTWARE: SeqWin99, version 1.04
, SEQ ID NO 7860
, LENGTH: 134
, TYPE: PR1
, ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7860

Query Match      38.7%; Score 41; DB 6; Length 134;
Best Local Similarity 72.7%; Pred. No. 5.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GVLLKGGKREBEK 16
Db 16 GVLLRGTKRED 26

RESULT 6
US-10-467-657-7966
, Sequence 7966, Application US/10/467657
, Publication No. US20050260581A1
, GENERAL INFORMATION:
, APPLICANT: CHIRON Spa
, APPLICANT: FONTANA Maria Rita
, APPLICANT: PIZZA Mariagrazia
, APPLICANT: MASIGNANI Vega
, APPLICANT: MONACI Elisabetta
, TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
, FILE REFERENCE:
, CURRENT APPLICATION NUMBER: US/10/467,657
, CURRENT FILING DATE: 2003-08-11
, PRIOR APPLICATION NUMBER: GB-0103424.8
, PRIOR FILING DATE: 2001-02-12
, NUMBER OF SEQ ID NOS: 9218
, SOFTWARE: SeqWin99, version 1.04
, SEQ ID NO 7966
, LENGTH: 394
, TYPE: PR1
, ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7966

Query Match      38.7%; Score 41; DB 6; Length 394;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      6 GVLKGGKREE 16
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Db     276 GVLKGGTKRED 286

RESULT 7
US-11-082-389-96
; Sequence 96, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ*ID NO 96
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-96

      Query Match      38.7%; Score 41; DB 7; Length 412;
      Best Local Similarity 70.0%; Pred. No. 19;
      Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 KEGVLLKGGK 13
      |||||:||||
Db     67 KDGVLKGGGE 76

RESULT 8
US-10-632-150-40
; Sequence 40, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chitaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LICASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27

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; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-40

      Query Match      37.7%; Score 40; DB 6; Length 257;
      Best Local Similarity 46.7%; Pred. No. 17;
      Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2 CTKEGVLLKGGKREE 16
      |||||:||||
Db     53 CQOEGVLPEGGVEEE 67

RESULT 9
US-11-073-457-40
; Sequence 40, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFER
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-40

      Query Match      37.7%; Score 40; DB 7; Length 257;
      Best Local Similarity 46.7%; Pred. No. 17;
      Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2 CTKEGVLLKGGKREE 16
      |||||:||||
Db     53 CQOEGVLPEGGVEEE 67

RESULT 10
US-11-073-460-40
; Sequence 40, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFER
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40

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! LENGTH: 257  
! TYPE: PRT  
! ORGANISM: Homo sapiens  
US-11-073-460-40

Query Match 37.7%; Score 40; DB 7; Length 257;  
Best Local Similarity 46.7%; Pred. No. 17;  
Matches 7; Conservative 4; Mismatches 4; Indels 4; Gaps 0;

Qy 2 CTKEGVLLKGGKREE 16  
| : || : : || ||  
Db 53 CQOEGVLPEGGVEEE 67

## RESULT 11

US-11-057-047-3  
; Sequence 3, Application US/11057047  
; Publication No. US20050260198A1  
; GENERAL INFORMATION:  
; APPLICANT: Holers, Vernon  
; APPLICANT: Thurman, Joshua  
; APPLICANT: Taube, Christian  
; APPLICANT: Gelfand, Erwin  
; APPLICANT: Gilkeson, Gary  
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and  
; TITLE OF INVENTION: Methods Related Thereto  
; FILE REFERENCE: 2848-66  
; CURRENT APPLICATION NUMBER: US/11/057.047  
; PRIOR FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,594  
; PRIOR FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: 60/636,239  
; PRIOR FILING DATE: 2004-12-14  
; PRIOR APPLICATION NUMBER: US04/015040  
; PRIOR FILING DATE: 2004-05-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-057-047-3

Query Match 36.8%; Score 39; DB 7; Length 70;  
Best Local Similarity 63.6%; Pred. No. 6.1;  
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

Qy 2 CTKEGVLLKGG 12  
| : || : : || ||  
Db 7 CSLEGEVIEKGG 17

## RESULT 12

US-10-131-826A-280  
; Sequence 280, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William

! APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 280  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-280

Query Match 36.8%; Score 39; DB 6; Length 245;  
Best Local Similarity 43.8%; Pred. No. 23;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 KEGVLLKGGKREBEKP 19  
| : || : : || ||  
Db 175 KEGIMKGNHVKNKP 190

## RESULT 13

US-11-057-047-2  
; Sequence 2, Application US/11057047  
; Publication No. US20050260198A1  
; GENERAL INFORMATION:  
; APPLICANT: Holers, Vernon  
; APPLICANT: Thurman, Joshua  
; APPLICANT: Taube, Christian  
; APPLICANT: Gelfand, Erwin  
; APPLICANT: Gilkeson, Gary  
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and  
; TITLE OF INVENTION: Methods Related Thereto  
; FILE REFERENCE: 2848-66  
; CURRENT APPLICATION NUMBER: US/11/057.047  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,594  
; PRIOR FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: 60/636,239  
; PRIOR FILING DATE: 2004-12-14  
; PRIOR APPLICATION NUMBER: US04/015040  
; PRIOR FILING DATE: 2004-05-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 739  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-057-047-2

Query Match 36.8%; Score 39; DB 7; Length 739;

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Best Local Similarity 63.6%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
Db 12 CSLEGVEIKGG 22

RESULT 14
US-11-057-047-6
; Sequence 6, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-057-047-6

Query Match 36.8%; Score 39; DB 7; Length 761;
Best Local Similarity 63.6%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
Db 34 CSLEGVEIKGG 44

RESULT 15
US-11-057-047-1
; Sequence 1, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-11-057-047-1

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Query Match 36.8%; Score 39; DB 7; Length 764;
Best Local Similarity 63.6%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 CTKEGVLLKGG 12
Db 37 CSLEGVEIKGG 47
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Search completed: December 29, 2005, 15:42:06
Job time : 14 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 15:30:06 ; Search time 37 Seconds  
(without alignments)  
52.009 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREKPKF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	46.2	658	2 B86599	metal transport P-
2	49	46.2	658	2 D72026	metal transport p-
3	49	46.2	659	2 A81742	cation-transportin
4	49	46.2	659	2 B71479	probable metal tra
5	49	46.2	683	2 C81515	cation-transportin
6	47	44.3	673	2 AG3521	cation-transportin
7	47	44.3	927	1 JQ0948	A5 antigen precurs
8	46.5	43.9	591	1 SYHUTP	CTP synthase (SC 6
9	46	43.4	389	2 S01371	myosin heavy chain
10	45	42.5	168	2 JG0184	fibroblast growth
11	45	42.5	257	2 E71601	probable integrin
12	45	42.5	450	2 S15675	globulin-2 precurs
13	44	41.5	97	2 T29766	hypothetical prote
14	44	41.5	141	2 T48751	hypothetical prote
15	44	41.5	154	2 T20508	hypothetical prote
16	44	41.5	228	2 C81184	conserved hypotet
17	44	41.5	281	2 B81440	acetylglutamate ki
18	44	41.5	396	2 A48336	coat protein - Sou
19	44	41.5	406	1 A70015	probable NADH2 deh
20	44	41.5	486	2 S63384	hypothetical prote
21	43	40.6	216	2 A56861	peptidylprolyl iso
22	43	40.6	227	2 F90249	ribiose 5-phosphate
23	43	40.6	394	2 H97825	elongation factor
24	43	40.6	394	2 C71672	translation elonga
25	43	40.6	416	2 H69436	5-enolpyruvylshiki
26	43	40.6	477	2 T52382	zinc finger protei
27	43	40.6	504	2 T10698	legumin-like prote
28	43	40.6	590	2 C81911	nitrate/nitrite se
29	43	40.6	590	2 B81104	nitrate/nitrite se

ALIGNMENTS

RESULT 1

B86599

metal transport P-type ATPase [imported] - Chlamydothila pneumoniae (strain J138)  
C;Species: Chlamydothila pneumoniae, Chlamydia pneumoniae  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: B86599  
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise  
Nucleic Acids Res. 28, 2311-2314, 2000  
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A;Reference number: A86491; MUID:20330349; PMID:10871362  
A;Accession: B86599  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-658 <STO>  
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:BA000008; NID:98979242; PFI  
A;Experimental source: strain J138  
C;Genetics:  
A;Gene: zntA  
C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding do

Query Match 46.2%; Score 49; DB 2; Length 658;

Best Local Similarity 81.8%; Pred. No. 16;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12

Db 331 CAKHGVLLKGG 341

RESULT 2

D72026

metal transport P-type ATPase - Chlamydothila pneumoniae (strain CWL029)  
C;Species: Chlamydothila pneumoniae, Chlamydia pneumoniae  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: D72026  
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A;Reference number: A72000; MUID:99206606; PMID:10192388  
A;Accession: D72026  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-658 <ARN>  
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID  
A;Experimental source: strain CWL029  
C;Genetics:  
A;Gene: zntA

Query Match 46.2%; Score 49; DB 2; Length 658;

Best Local Similarity 81.8%; Pred. No. 16;

```

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
   |||||
Db 331 CAKHGVLLKGG 341

RESULT 3
A81742
cation-transporting ATPase, E1-E2 family TC0100 [imported] - Chlamydia muridarum (strain
C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: A81742
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: A81742
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-659 <TET>
A/Cross-references: UNIPROT:Q9PLJ9; UNIPARC:UPI00000577C9; GB:AE002277; GB:AE002160; NID
A/Experimental source: strain Nigg (MoPn)
C/Genetics:
A/Gene: TC0100
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F/478-620/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 659;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
   |||||
Db 331 CAKHGVLLKGG 341

RESULT 4
B71479
probable metal transport p-type ATPase - Chlamydia trachomatis (serotype D, strain UW3/C
C/Species: Chlamydia trachomatis
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C/Accession: B71479
R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Pan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A/Reference number: A71570; MUID:99000809; PMID:9784136
A/Accession: B71479
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-659 <ARN>
A/Cross-references: UNIPROT:O84732; UNIPARC:UPI000000D3395; GB:AE001343; GB:AE001273; NID
A/Experimental source: serotype D, strain UW-3/Cx
C/Genetics:
A/Gene: zntA
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F/64-400/Domain: ATPase nucleotide-binding domain homology <ATP>
F/478-620/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 659;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
   |||||
Db 331 CAKHGVLLKGG 341

RESULT 5
C81515
cation-transporting ATPase, E1-E2 family CP1001 [imported] - Chlamydia pneumoniae (s
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

```

```

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: C81515
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: C81515
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-683 <REA>
A/Cross-references: UNIPROT:Q9K1U0; UNIPARC:UPI000000CCCD4; GB:AE002257; GB:AE002161; NID
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: CP1001
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F/503-645/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 683;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
   |||||
Db 356 CAKHGVLLKGG 366

RESULT 6
AG3521
cation-transporting p-type ATPase b (EC 3.6.1.1-) [imported] - Brucella melitensis (strain
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: AG3521
R/DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Leteser
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A/Reference number: AD3252; PMID:11756688
A/Accession: AG3521
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-673 <KUR>
A/Cross-references: UNIPROT:Q8YDS8; UNIPARC:UPI0000058350; GB:AE008918; PIDN:AAL53338.1;
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BMEI10097
A/Map position: 11
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
C/Keywords: hydrolase

Query Match 44.3%; Score 47; DB 2; Length 673;
Best Local Similarity 56.2%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREE 16
   :|||:
Db 337 VCARGVLFKGGKALE 352

RESULT 7
JQ0948
A5 antigen precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: JH0466; JQ0948
R/Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A/Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homologi
A/Reference number: JH0466; MUID:91337458; PMID:1908252
A/Accession: JH0466
A/Molecule type: mRNA
A/Residues: 1-927 <TAK>
A/Cross-references: UNIPARC:UPI00000171502; GB:D10467; GB:D01077; NID:g222962; PIDN:BA001

```

A;Experimental source: tadpole, brain  
A;Note: this protein has motifs homologous to complement components C1r and C1s and to c...  
C;Comment: This protein is a neuronal cell surface molecule involved in the neuronal re...  
C;Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal h...  
C;Keywords: duplication; glycoprotein; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-927/Product: A5 antigen #status predicted <ASA>  
F;27-138/Domain: C1r/C1s repeat homology <C1R1>  
F;147-262/Domain: C1r/C1s repeat homology <C1R2>  
F;274-424/Domain: discoidin I amino-terminal homology <DN1>  
F;430-584/Domain: discoidin I amino-terminal homology <DN2>  
F;646-812/Domain: MAM homology <MAM>  
F;861-883/Domain: transmembrane #status predicted <TM>  
F;150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.3%; Score 47; DB 1; Length 927;  
Best Local Similarity 53.3%; Pred. No. 44;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 GVLLKGGKREEEKP 20  
DB 498 GVIIQGGKHENKVF 512  
|||||:|:|

RESULT 8  
SYHUTP  
C;Title: CTP synthase (EC 6.3.4.2) - human  
N;Alternate names: CTP-synthetase; UTP-ammonia ligase  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: S12791  
R;Yamauchi, M.; Yamauchi, N.; Meuth, M.  
EMBO J. 9, 2095-2099, 1990  
A;Title: Molecular cloning of the human CTP synthetase gene by functional complementatio...  
A;Reference number: S12791; MUID:90291972; PMID:2113467  
A;Accession: S12791  
A;Molecule type: mRNA  
A;Residues: 1-591 <YAM>  
A;Cross-references: UNIPROT:P17812; UNIPARC:UPI0000163BFD; GB:X52142; NID:g30292; PIDN:C...  
C;Comment: This enzyme is a glutamine amidotransferase that catalyzes the terminal react...  
C;Genetics:  
A;Gene: GDB:CTPS  
A;Cross-references: GDB:126729; OMIM:123860  
A;Map position: lp34.3-1p34.1  
C;Superfamily: CTP synthase  
C;Keywords: ligase; pyrimidine nucleotide biosynthesis

Query Match 43.9%; Score 46.5; DB 1; Length 591;  
Best Local Similarity 31.4%; Pred. No. 35;  
Matches 11; Conservative 4; Mismatches 5; Indels 15; Gaps 1;

QY 1 LCTKEGVLLKGG-----KREEEKP 20  
DB 361 LCSAHGVLPFGVGTGKQIAIARWNRQKPF 395  
|||||:|:|

RESULT 9  
S01371  
myosin heavy chain, cardiac and skeletal muscle - eastern newt (fragment)  
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)  
C;Date: 30-Sep-1989 #sequence\_revision 06-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: S01371; S67907  
R;Casimir, C.M.; Gates, P.B.; Ross-Macdonald, P.B.; Jackson, J.F.; Patient, R.K.; Brocke...  
J. Mol. Biol. 202, 287-296, 1988  
A;Title: Structure and expression of a newt cardio-skeletal myosin gene. Implications fo...  
A;Reference number: S01371; MUID:89011957; PMID:2459393  
A;Accession: S01371  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-171 <CAS>  
A;Cross-references: UNIPROT:Q7LZ84; UNIPARC:UPI0000177608  
A;Note: the sequence from fig. 7 is inconsistent with that from fig. 5 in having 64-Ile,  
A;Accession: S67907

A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 36-389 <CAS2>  
A;Cross-references: UNIPARC:UPI0000177609  
A;Note: the sequence from fig. 7 is inconsistent with that from fig. 5 in having 64-Ile,  
C;Superfamily: myosin heavy chain; myosin motor domain homology  
C;Keywords: ATP; cardiac muscle; coiled coil; heart; muscle contraction; skeletal muscle,  
Query Match 43.4%; Score 46; DB 2; Length 389;  
Best Local Similarity 44.4%; Pred. No. 28;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREEEK 18  
DB 249 LMEAEQIAMKGGKKQEQK 266  
|||||:|:|

RESULT 10  
JG0184  
fibroblast growth factor - human  
C;Species: Homo sapiens (man)  
C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: JG0184  
R;Kok, L.D.S.; Tsui, S.K.W.; Waye, M.; Liew, C.C.; Lee, C.Y.; Fung, K.P.  
Biochem. Biophys. Res. Commun. 255, 717-721, 1999  
A;Title: Cloning and characterization of a cDNA encoding a novel fibroblast growth factor  
A;Reference number: JG0184; MUID:99160419; PMID:10049777  
A;Accession: JG0184  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-168 <KOK>  
A;Cross-references: UNIPROT:P61328; UNIPARC:UPI0000040663; GB:U76381  
C;Superfamily: fibroblast growth factor

Query Match 42.5%; Score 45; DB 2; Length 168;  
Best Local Similarity 50.0%; Pred. No. 18;  
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 KEGVLLKGGKREEEKP 19  
DB 117 KEGQIMKGNRVKTKP 132  
|||||:|:|

RESULT 11  
E71601  
probable integral membrane protein PFB0995w - malaria parasite (Plasmodium falciparum)  
C;Species: Plasmodium falciparum  
C;Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004  
C;Accession: E71601  
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;  
Science 282, 1126-1132, 1998  
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A;Reference number: A71600; MUID:99021743; PMID:9804551  
A;Accession: E71601  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-257 <GAR>  
A;Cross-references: UNIPROT:Q9TY93; UNIPARC:UPI00000814CB; GB:AE001431; GB:AE001362; NID:  
A;Experimental source: clone 3D7  
C;Genetics:  
A;Gene: PFB0995w

Query Match 42.5%; Score 45; DB 2; Length 257;  
Best Local Similarity 50.0%; Pred. No. 27;  
Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 4 KEGVLLK-----GGKREEEKP 19  
DB 11 KSGVLLKDKNTEBGRKKRQKP 32  
|||||:|:|

RESULT 12

S15675  
 globulin-2 precursor - maize  
 C/Species: Zea mays (maize)  
 C/Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C/Accession: S15675  
 R/Mallace, N.H.; Kriz, A.L.  
 A/Title: Nucleotide sequence of a cDNA clone corresponding to the maize globulin-2 gene.  
 A/Reference number: S15675  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-450 <WAL>  
 A/Cross-references: UNIPROT:Q7M1Z8; UNIPARC:UPI00000177E41  
 C/Superfamily: vicilin

Query Match 42.5%; Score 45; DB 2; Length 450;  
 Best Local Similarity 68.8%; Pred. No. 45;  
 Matches 11; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

Qy . 4 KEG-----VLLKGGKRE 15  
 Db 95 KEGGVIVLLRGGKRE 110  
 ||||| :|||:|||||  
 ||||| :|||:|||||

RESULT 13  
 T29766  
 hypothetical protein ZC581.5 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C/Accession: T29766  
 R/Waterston, B.; Gattung, S.; Le, T.T.  
 A/Description: The sequence of C. elegans cosmid ZC581.  
 A/Reference number: Z20682  
 A/Accession: T29766  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-97 <WAT>  
 A/Cross-references: UNIPARC:UPI000017BCE4; EMBL:AF003134; PIDN:AAB54143.1; GSPDB:GN000019  
 A/Experimental source: strain Bristol N2; clone ZC581  
 C/Genetics:  
 A/Gene: CESP:ZC581.5  
 A/Map position: 1  
 A/Introns: 74/1

Query Match 41.5%; Score 44; DB 2; Length 97;  
 Best Local Similarity 53.8%; Pred. No. 15;  
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 EGVLLKGGKRE 17  
 Db 31 ERIIMKGGKNEED 43  
 ||||| :|||:|||||  
 ||||| :|||:|||||

RESULT 14  
 T48751  
 hypothetical protein 8D4.250 [imported] - Neurospora crassa  
 C/Species: Neurospora crassa  
 C/Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 19-May-2000  
 C/Accession: T48751  
 R/Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
 A/Submitted to the Protein Sequence Database, April 2000  
 A/Reference number: Z24541  
 A/Accession: T48751  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-141 <SCH>  
 A/Cross-references: UNIPARC:UPI0000179478; EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.250  
 A/Experimental source: cosmid contig 8D4; strain 74  
 C/Genetics:  
 A/Gene: NCSP:8D4.250  
 A/Map position: 2

C/Superfamily: Neurospora crassa hypothetical protein 8D4.250

Query Match 41.5%; Score 44; DB 2; Length 141;  
 Best Local Similarity 64.3%; Pred. No. 21;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TKEGVLLKGGKRE 16

Db 74 TNGKLLSGKDDE 87

RESULT 15

T20508

hypothetical protein F02E9.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T20508

R/Gray, I.

A/Submitted to the EMBL Data Library, November 1996

A/Reference number: Z19285

A/Accession: T20508

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-154 <WIL>

A/Cross-references: UNIPROT:O01314; UNIPARC:UPI0000074F98; EMBL:Z81494; PIDN:CAB04047.1;

A/Experimental source: clone F02E9

C/Genetics:

A/Gene: CESP:F02E9.1

A/Map position: 1

A/Introns: 29/2; 52/2; 80/3; 131/3

Query Match 41.5%; Score 44; DB 2; Length 154;

Best Local Similarity 60.0%; Pred. No. 23;

Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 1 LCTKEG--VLLKGGKRE 18

Db 53 LDTKNGKFVLLKNSENE 72

Search completed: December 29, 2005, 15:40:56

Job time : 38 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 15:29:18 ; Search time 230 Seconds  
(without alignments)  
61.350 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREBEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	159	2 Q5YLW1_HUMAN	Q5YLW1 homo sapien
2	106	100.0	498	1 ANGPI1_HUMAN	Q15389 homo sapien
3	106	100.0	498	1 ANGPI1_MOUSE	O08538 mus musculus
4	106	100.0	498	2 Q5HYA0_HUMAN	Q5HYA0 homo sapien
5	106	100.0	498	2 Q6NWX7_MOUSE	Q6NWX7 mus musculus
6	106	100.0	498	2 Q8C2K6_MOUSE	Q8C2K6 mus musculus
7	96	90.6	498	2 Q9BDY8_PIG	Q9BDY8 sus scrofa
8	89.5	84.4	147	2 Q8N6P3_HUMAN	Q8N6P3 homo sapien
9	89.5	84.4	497	1 ANGPI1_RAT	Q35460 rattus norv
10	89.5	84.4	521	2 Q6A0F0_MOUSE	Q6A0F0 mus musculus
11	86.5	81.6	497	2 Q60FC1_CANFA	Q60FC1 canis fami
12	85.5	80.7	481	1 ANGPI1_BOVIN	O18920 bos taurus
13	76	71.7	504	2 Q6GNY4_XENLA	Q6GNY4 xenopus lae
14	59	55.7	383	2 Q9CUL6_MOUSE	Q9CUL6 mus musculus
15	55	51.9	178	2 Q4RN08_TETNG	Q4RN08 tetraodon n
16	54	50.9	1040	2 Q8H7M2_ORYSA	Q8H7M2 oryza sativ
17	53	50.0	890	2 Q8B488_FFLAV	Q8B488 iguape viru
18	52.5	49.5	591	2 Q5XHA8_XENLA	Q5XHA8 xenopus lae
19	51	48.1	181	2 Q816J1_CIOSA	Q816J1 ciona savig
20	51	48.1	273	2 Q9CST2_MOUSE	Q9CST2 mus musculus
21	51	48.1	566	2 Q7Y188_ORYSA	Q7Y188 oryza sativ
22	51	48.1	691	2 Q7Y017_ORYSA	Q7Y017 oryza sativ
23	51	48.1	940	2 Q7XDX7_ORYSA	Q7XDX7 oryza sativ
24	51	48.1	974	2 Q6L423_ORYSA	Q6L423 oryza sativ
25	51	48.1	982	2 Q7XWN4_ORYSA	Q7XWN4 oryza sativ
26	51	48.1	1059	2 Q60E55_ORYSA	Q60E55 oryza sativ
27	51	48.1	1109	2 Q5KQJ6_ORYSA	Q5KQJ6 oryza sativ
28	51	48.1	1177	2 Q75J33_ORYSA	Q75J33 oryza sativ
29	51	48.1	1180	2 Q75HCL_ORYSA	Q75HCL oryza sativ
30	51	48.1	1198	2 Q6L559_ORYSA	Q6L559 oryza sativ
31	51	48.1	1198	2 Q94GS7_ORYSA	Q94GS7 oryza sativ

32 51 48.1 1224 2 Q84TW9\_ORYSA Q84TW9 oryza sativ  
33 51 48.1 1225 2 Q5TKC1\_ORYSA Q5TKC1 oryza sativ  
34 51 48.1 1229 2 Q6I578\_ORYSA Q6I578 oryza sativ  
35 51 48.1 1264 2 Q7XP54\_ORYSA Q7XP54 oryza sativ  
36 51 48.1 1264 2 Q8LSK0\_MAIZE Q8LSK0 zea mays (m  
37 51 48.1 1274 2 Q9FW32\_ORYSA Q9FW32 oryza sativ  
38 51 48.1 1277 2 Q53KA0\_ORYSA Q53KA0 oryza sativ  
39 51 48.1 1282 2 Q7XRW0\_ORYSA Q7XRW0 oryza sativ  
40 51 48.1 1289 2 Q60E18\_ORYSA Q60E18 oryza sativ  
41 51 48.1 1297 2 Q6L563\_ORYSA Q6L563 oryza sativ  
42 51 48.1 1297 2 Q7XP63\_ORYSA Q7XP63 oryza sativ  
43 51 48.1 1297 2 Q6L4G8\_ORYSA Q6L4G8 oryza sativ  
44 51 48.1 1302 2 Q6L5B9\_ORYSA Q6L5B9 oryza sativ  
45 51 48.1 1302 2 Q75J10\_ORYSA Q75J10 oryza sativ

#### ALIGNMENTS

RESULT 1  
Q5YLW1\_HUMAN PRELIMINARY; PRT; 159 AA.  
AC Q5YLW1\_  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Angiopietin-A.  
GN Names=AngA;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Wang H., Zhang Y., Liang H.C., Zhang M., Sun D.H., Wang B.,  
RA Zhang G.Z.;  
RT "The Expression of Angiopietin-A During Vascular Development.";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY055342; AAL59669.1; -; mRNA.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
SQ SEQUENCE 159 AA; 18221 MW; F129DA56FB6AFC66 CRC64;

Query Match 100.0%; Score 106; DB 2; Length 159;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEKPF 20  
|||||  
Db 77 LCTKEGVLLKGGKREBEKPF 96

RESULT 2  
ANGPI1\_HUMAN STANDARD; PRT; 498 AA.  
AC Q15389;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Angiopietin-1 precursor (ANG-1).  
GN Name=ANGPT1; Synonyms=KIAA0003;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.  
RC TISSUE=Petal lung;  
RX MEDLINE=97134663; PubMed=8980223; DOI=10.1016/S0092-8674(00)81812-7;  
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,  
RA Ryan T.E., Bruno J., Radziejewski C., Maisonnier P.C.,

RA Yancopoulos G.D.;  
 RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by  
 RT secretion-trap expression cloning.";   
 RL Cell 87:1161-1169(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.  
 RA Nakatukasa M., Komai K., Shiozawa S.;  
 RT "Human angiopoietin-1 mRNA variant form.";   
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.  
 RA Shan Z.X., Yu X.Y., Lin Q.Y., Fu Y.H., Tan H.H., Zheng M., Lin S.G.;  
 RT "Human angiopoietin-1 mRNA variant forms.";   
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TIGR-Bone marrow;  
 RX MIM:6051387; PubMed=7584026;  
 RA Namura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,  
 RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.,  
 RT "Prediction of the coding sequences of unidentified human genes. I.  
 RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
 RT analysis of randomly sampled cDNA clones from human immature myeloid  
 RT cell line KG-1.";   
 RL DNA Res. 1:27-35(1994).  
 RN [5]  
 RP SEQUENCE REVISION.  
 RX MEDLINE=22158633; PubMed=12168954;  
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual  
 RT curation of 330 KIAA cDNA clones.";   
 RL DNA Res. 9:93-106(2002).  
 CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its  
 CC tyrosine phosphorylation. Implicated in endothelial developmental  
 CC processes later and distinct from that of VEGF. Appears to play a  
 CC crucial role in mediating reciprocal interactions between the  
 CC endothelium and surrounding matrix and mesenchyme. Mediates blood  
 CC vessel maturation/stability. It may play an important role in the  
 CC heart early development.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Glycosylated.  
 CC It can be used for specifically targeting tumor vasculature or for  
 CC promoting angiogenic processes in certain organs such as an  
 CC ischemic heart.  
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; U83508; AAB50557.1; -; mRNA.  
 DR EMBL; AB084454; BAB91325.1; -; mRNA.  
 DR EMBL; AY121504; AAB81745.1; -; mRNA.  
 DR EMBL; AY144360; AAB52271.1; -; mRNA.  
 DR EMBL; D13628; BAA02793.2; ALT\_INIT; mRNA.  
 DR HSSP; P02671; 1FZD.  
 DR Ensembl; ENSG00000154188; Homo sapiens.  
 DR HGNC; HGNC:484; ANGPT1.  
 DR H-InvDB; HIX000720; -.  
 DR MIM; 601667; -.  
 DR GO; GO:0005102; F:receptor binding; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR002181; Fibrinogen\_C.  
 DR Pfam; PF00147; Fibrinogen\_C; 1.  
 DR SMART; SM00186; FBG; 1.  
 DR PROSITE; PS00514; FIBRIN AG C-DOMAIN; 1.  
 DR Angiogenesis; Coiled coil; Developmental protein; Differentiation;  
 KW Glycoprotein; Polymorphism; Signal.  
 FT SIGNAL 1 15  
 FT CHAIN 16 498 Angiopoietin-1.

FT DOMAIN 284 498 Fibrinogen C-terminal.  
 FT COILED 81 119 Potential.  
 FT COILED 153 261 Potential.  
 FT CARBOHYD 92 92 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 122 122 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 154 154 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 243 243 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 295 295 N-linked (GlcNAc... ) (Potential).  
 FT DISULFID 286 315 By similarity.  
 FT DISULFID 439 452 Missing (in cell line T98G; may be due to  
 FT VARIANT 269 269 exon slippage).  
 FT /FTID=VAR\_009940.  
 SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;  
 Query Match 100.0%; Score 105; DB 1; Length 498;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LCTKEGVLLKGGKREBEKPF 20  
 DQ 264 LCTKEGVLLKGGKREBEKPF 283  
 RESULT 3  
 ANGPT1\_MOUSE STANDARD; PRT; 498 AA.  
 ID ANGPT1\_MOUSE  
 AC Q08538;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Angiopoietin-1 precursor (ANG-1).  
 GN Name-Angpt1; Synonyms-Angpt;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Murinae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=97134663; PubMed=8980223; DOI=10.1016/S0092-8674(00)81812-7;  
 RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,  
 RA Ryan T.E., Bruno J., Radziejewski C., Maisonnier P.C.,  
 RA Yancopoulos G.D.;  
 RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by  
 RT secretion-trap expression cloning.";   
 RL Cell 87:1161-1169(1996).  
 CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its  
 CC tyrosine phosphorylation. Implicated in endothelial developmental  
 CC processes later and distinct from that of VEGF. Appears to play a  
 CC crucial role in mediating reciprocal interactions between the  
 CC endothelium and surrounding matrix and mesenchyme. Mediates blood  
 CC vessel maturation/stability. It may play an important role in the  
 CC heart early development.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DEVELOPMENTAL STAGE: Early in development, at E9 to E11, it is  
 CC found most prominently in the heart myocardium surrounding the  
 CC endocardium. Later, it becomes more widely distributed, most often  
 CC in the mesenchyme surrounding developing vessels, in close  
 CC association with endothelial cells.  
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; U83508; AAB50557.1; -; mRNA.  
 DR HSSP; P02671; 1FZD.  
 DR Ensembl; ENSMUSG000000022309; Mus musculus.  
 DR MGI; MGI:108448; Angpt1.  
 DR GO; GO:0005615; C:extracellular space; TAS.

```
DR GO: 0005172; F:vascular endothelial growth factor receptor. . . ; TAS.
DR GO: 0007492; P:endothelium development; TAS.
DR GO: 0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.
KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
KW Glycoprotein; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 498 Angiopoietin-1.
FT DOMAIN 284 498 Fibrinogen C-terminal.
FT COILED 81 119 Potential.
FT COILED 153 261 Potential.
FT CARBOHYD 92 92 N-linked (GlcNAc. . . ) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc. . . ) (Potential).
FT CARBOHYD 154 154 N-linked (GlcNAc. . . ) (Potential).
FT CARBOHYD 243 243 N-linked (GlcNAc. . . ) (Potential).
FT CARBOHYD 295 295 N-linked (GlcNAc. . . ) (Potential).
FT DISULFID 286 315 By similarity.
FT DISULFID 439 452 By similarity.
SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC260D800 CRC64;

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
DB 264 LCTKEGVLKGGKREBEKPF 283

RESULT 4
QSHYAO HUMAN
ID QSHYAO HUMAN PRELIMINARY; PRT; 498 AA.
AC QSHYAO
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DEL Hypothetical protein DKFZp686L10222.
GN Name=DKFZp686L10222;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX648814; CAI45984.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;

Query Match 100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
DB 264 LCTKEGVLKGGKREBEKPF 283

RESULT 5
Q6NWV7 MOUSE
ID Q6NWV7 MOUSE PRELIMINARY; PRT; 498 AA.
AC Q6NWV7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

```
DE Angiopoietin 1.
GN Name=Angptl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RG STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wegner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Zordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleto M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RG STRAIN=C57BL/6J; TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067410; AAH67410.1; -; mRNA.
DR GO: 0005615; C:extracellular space; TAS.
DR GO: 0005172; F:vascular endothelial growth factor receptor. . . ; TAS.
DR GO: 0007492; P:endothelium development; TAS.
DR GO: 0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.
SQ SEQUENCE 498 AA; 57519 MW; FC36F905A9E79074 CRC64;

Query Match 100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
| | | | | | | | | | | | | | | | | | | | | |
DB 264 LCTKEGVLKGGKREBEKPF 283

RESULT 6
Q8C2K6 MOUSE
ID Q8C2K6 MOUSE PRELIMINARY; PRT; 498 AA.
AC Q8C2K6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
DE length enriched library, clone:E430016L03 product:angiopoietin, full
DE insert sequence.
GN Name=Angptl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```



RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Akazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikolaou I., Pesole G., Quackenbush J.,  
RA Schram L.M., Staehli P., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu N., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NOD; TISSUE=Thymus;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanegaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submittet (Apr-2002) to the EMBL/GenBank/DBJ databases.  
DR ENBL; AK088439; BAC40354.1; -, mRNA.  
DR HSSP; P02671; IPZD.  
DR MGI; MGI:108448; Angptl.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
DR SMART; SM00186; FBG; 1.  
DR PROSITE; PS00514; FIBRIN AG\_C DOMAIN; 1.  
SQ SEQUENCE 498 AA; 57475 MW; 285D957466C5D800 CRC64;  
Query Match 100.0%; Score 106; DB 2; Length 498;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LCTKEGVLKGGKREBEKPF 20  
Db 264 LCTKEGVLKGGKREBEKPF 283  
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RESULT 7  
Q9BDY8\_PIG PRELIMINARY; PRT; 498 AA.  
ID Q9BDY8\_PIG PRELIMINARY;  
AC Q9BDY8;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Angiopoietin 1.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21153163; PubMed=11230987; DOI=10.1016/S0008-6363(00)00295-9;  
RA Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;  
RT "The angiotensin-tie2 system in coronary artery endothelium prevents  
RT oxidized low-density lipoprotein-induced apoptosis.";  
RL Cardiovasc. Res. 49:872-881(2001).  
DR ENBL; AF233227; AAK14992.1; -, mRNA.  
DR HSSP; P02671; IPZD.  
DR GO; GO:0001525; P:angiogenesis; IEA.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
DR SMART; SM00186; FBG; 1.  
DR PROSITE; PS00514; FIBRIN AG\_C DOMAIN; 1.  
SQ SEQUENCE 498 AA; 57413 MW; A8C1C8EF56061876 CRC64;  
Query Match 90.6%; Score 96; DB 2; Length 498;  
Best Local Similarity 90.0%; Pred. No. 6e-06;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 LCTKEGVLKGGKREBEKPF 20  
Db 264 LCTKEGVLKGGKREBEKPF 283  
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RESULT 8  
Q8N6P3\_HUMAN PRELIMINARY; PRT; 147 AA.  
ID Q8N6P3\_HUMAN PRELIMINARY;  
AC Q8N6P3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE ANGPT1 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Prostate;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heish F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Beasak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Prostate;  
 RA Strauberg R.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC029406; AAH29406.1; -; mRNA.  
 DR HSPSP; P02671; lFZD.  
 DR InterPro; IPR002181; Fibrinogen\_C.  
 DR Pfam; PF00147; Fibrinogen\_C; 1.  
 DR SMART; SM00186; FBG; 1.  
 SQ SEQUENCE 147 AA; 17314 MW; 68DFD40DE06FA37E CRC64;

Query Match 84.4%; Score 89.5; DB 1; Length 147;  
 Best Local Similarity 95.0%; Pred. No. 1.8e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLLKGGKREBEKPF 20  
 ||||| ||||| ||||| ||||| |||||  
 DB 10 LCTKE-VLLKGGKREBEKPF 28

RESULT 9  
 ANGLP1\_RAT  
 ID ANGLP1\_RAT STANDARD; PRT; 497 AA.  
 AC Q35460; Q8K4Q4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Angiopoietin-1 precursor (ANG-1).  
 GN Name=Angpt1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=WiStar; TISSUE=Placenta;  
 RX MEDLINE=22346496; PubMed=12458684; DOI=10.1023/A:1020921818105;  
 RA Iizasa H., Bae S.H., Asashima T., Kitano T., Matsunaga N.,  
 RA Terasaki T., Kang Y.S., Nakashima E.;  
 RT "Augmented expression of the tight junction protein occludin in brain  
 RT endothelial cell line TR-BBB by rat angiopoietin-1 expressed in  
 RT baculovirus-infected sf plus insect cells.";  
 RL Pharm. Res. 19:1757-1760 (2002).  
 RN [2]

RP NUCLEOTIDE SEQUENCE OF 91-200.  
 RC STRAIN=Sprague-Dawley; TISSUE=Placenta;  
 RX MEDLINE=98451564; PubMed=9776732;  
 RA Mandriota S.J., Pepper M.S.;

RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular  
 RT endothelial cells by cytokines and hypoxia.";  
 RL Circ. Res. 83:852-859 (1998).  
 CC -I- FUNCTION: Binds and activates Tie2 receptor by inducing its  
 CC tyrosine phosphorylation. Implicated in endothelial developmental  
 CC processes later and distinct from that of VEGF. Appears to play a  
 CC crucial role in mediating reciprocal interactions between the  
 CC endothelium and surrounding matrix and mesenchyme. Mediates blood  
 CC vessel maturation/stability. It may play an important role in the  
 CC heart early development.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: Contains 1 fibrinogen C-terminal domain.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; AB080023; BAC10290.1; -; mRNA.  
 DR EMBL; AF030376; AAC78246.1; -; mRNA.  
 DR HSPSP; P02671; lFZD.  
 DR Ensembl; ENSRNOG00000005854; Rattus norvegicus.  
 DR RGD; 628896; Angpt1.  
 DR GO; GO:0005102; P:receptor binding; TAS.  
 DR GO; GO:0001525; P:angiogenesis; IEP.  
 DR GO; GO:0048014; P:Tie receptor signaling pathway; IDA.  
 DR InterPro; IPR002181; Fibrinogen\_C.  
 DR Pfam; PF00147; Fibrinogen\_C; 1.  
 DR SMART; SM00186; FBG; 1.  
 DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; 1.  
 DR Angiogenesis; Coiled coil; Developmental protein; Differentiation;  
 KW Glycoprotein; Signal.  
 FT SIGNAL 1 19 Potential.  
 FT CHAIN 20 497 Angiopoietin-1.  
 FT DOMAIN 283 497 Fibrinogen C-terminal.  
 FT COILED 81 119 Potential.  
 FT CARBOHYD 153 261 Potential.  
 FT CARBOHYD 92 92 N-linked (GLNAC. . .) (Potential).  
 FT CARBOHYD 122 122 N-linked (GLNAC. . .) (Potential).  
 FT CARBOHYD 154 154 N-linked (GLNAC. . .) (Potential).  
 FT CARBOHYD 243 243 N-linked (GLNAC. . .) (Potential).  
 FT CARBOHYD 294 294 N-linked (GLNAC. . .) (Potential).  
 FT DISULFID 285 314 By similarity.  
 FT DISULFID 438 451 By similarity.  
 FT CONFLICT 98 98 Q -> E (in Ref. 2).  
 FT CONFLICT 172 172 E -> K (in Ref. 2).  
 FT CONFLICT 189 189 E -> K (in Ref. 2).  
 SQ SEQUENCE 497 AA; 57461 MW; 08E66ABEBF0869AE CRC64;

Query Match 84.4%; Score 89.5; DB 1; Length 497;  
 Best Local Similarity 95.0%; Pred. No. 6e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLLKGGKREBEKPF 20  
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 DB 264 LCTKE-VLLKGGKREBEKPF 282

RESULT 10  
 Q6A0F0\_MOUSE  
 ID Q6A0F0\_MOUSE PRELIMINARY; PRT; 521 AA.  
 AC Q6A0F0;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE MKIAA0003 protein (fragment).  
 GN Name=Angpt1; Synonyms=MKIAA0003;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

```

RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Adult spleen;
RX PubMed=15368895;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 11:205-218(2004).
DR EMBL; AK172868; BAD32146.1; -; mRNA.
DR MGI; MGI:108448; Angptl.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005172; F:vascular endothelial growth factor receptor. .; TAS.
DR GO; GO:0007492; P:endothelium development; TAS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
FT NON TER 1
SQ SEQUENCE 521 AA; 60103 MW; 8E7061F2A570EDFA CRC64;

Query Match 84.4%; Score 89.5; DB 2; Length 521;
Best Local Similarity 95.0%; Pred. No. 6.2e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGKREKPF 20
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Db 288 LCTKE-VLLKGGKREKPF 306

RESULT 11
ID Q60FC1 CANFA PRELIMINARY; PRT; 497 AA.
AC Q60FC1.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Angiopoietin-1.
GN Name=Ang-1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kato Y., Asano K.;
RT "Canis familiaris Angiopoietin-1 mRNA, complete cds.";
RL EMBL; AB192412; BAD54826.1; -; mRNA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 497 AA; 57415 MW; 061AFC2B03E8F081 CRC64;

Query Match 81.6%; Score 86.5; DB 2; Length 497;
Best Local Similarity 90.0%; Pred. No. 0.00017;
Matches 18; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGKREKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 264 LCTKE-VLLKGGKREKPF 282

RESULT 12
ANGP1_BOVIN
ID ANGP1_BOVIN STANDARD; PRT; 481 AA.

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AC Q18920;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1) (Fragment).
GN Name=ANGPT1; Synonyms=ANG1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=99054348; PubMed=9840613;
RA Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT angiogenesis.";
RL Lab. Invest. 78:1385-1394(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 91-200.
RC TISSUE=Liver;
RX MEDLINE=98451564; PubMed=9776732;
RA Mandiota S.J., Pepper M.S.;
RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859(1998).
CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its
CC tyrosine phosphorylation. Implicated in endothelial developmental
CC processes later and distinct from that of VEGF. Appears to play a
CC crucial role in mediating reciprocal interactions between the
CC endothelium and surrounding matrix and mesenchyme. Mediates blood
CC vessel maturation/stability. It may play an important role in the
CC heart early development (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: Found to be expressed throughout the ovarian
CC cycle.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF093573; AAC61872.1; -; mRNA.
DR EMBL; AF032923; AAC78245.1; -; mRNA.
DR HSP; Q9U8W8; IJC9.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
KW Glycoprotein; Signal.
FT SIGNAL 1 15
FT CHAIN 16 >481
FT DOMAIN 283 >481 Fibrinogen C-terminal.
FT COILED 153 261 Potential.
FT CARBOHYD 92 92 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 154 154 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 243 243 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 294 294 N-linked (GlcNAc. .) (Potential).
FT DISULFID 285 314 By similarity.
FT DISULFID 438 451 By similarity.
FT NON TER 481
SQ SEQUENCE 481 AA; 55557 MW; 8BEC9ED84FC2BB50 CRC64;

Query Match 80.7%; Score 85.5; DB 1; Length 481;
Best Local Similarity 90.0%; Pred. No. 0.00024;
Matches 18; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGKREKPF 20

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Db 264 LCTKE-VLLKGGKREKEKPF 282
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RESULT 13
Q6GN4_XENLA PRELIMINARY; PRT; 504 AA.
ID Q6GN4;
AC Q6GN4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4930463121 product:hypothetical protein, full insert
DE sequence. (Fragment).
GN Name=Armc4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=8355;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant J.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Sakai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyono-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Query Match 71.78; Score 76; DB 2; Length 504;
Best Local Similarity 70.08; Pred. No. 0.007;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 LCTKEGVLKGGKREKEKPF 20
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Db 270 LCSKEGTVKRVKREKPF 289
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Tanaka S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RL sequencing pipeline with 384 multipillar sequencer.",  
RN Genome Res. 10:1757-1771(2000).  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=Testis;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK015498; BAB29870.2; -; mRNA.  
DR Ensembl; ENSMUSG00000024280; Mus musculus.  
DR MGI; MGI:1922184; Armc4.  
KW Hypothetical protein.  
FT CON TER 383 383  
SQ SEQUENCE 393 AA; 43608 MW; AA688BA4AACB01D CRC64;

Query Match 55.7%; Score 59; DB 2; Length 383;  
Best Local Similarity 68.8%; Pred. No. 2.1;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGGKREE 17  
|: ||| | ||| |||  
Db 262 CSTGEVFLNGGKTEE 277

RESULT 15  
QARNQ8\_TETNG  
ID QARNQ8\_TETNG PRELIMINARY; PRT; 178 AA.  
AC QARNQ8;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome 2 SCAP15010, whole genome shotgun sequence.  
GN ORFNames=GSTENG00031451001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Desilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAE01015010; CAG09974.1; -; Genomic\_DNA.  
DR InterPro; IPR011700; bZIP\_2.  
DR InterPro; IPR004827; TF\_bZIP.  
DR Pfam; PF07716; bZIP\_2; 1.  
DR PROSITE; PS00217; bZIP; 1.  
DR PROSITE; PS00036; bZIP\_BASIC; 1.  
KW DNA-binding; Nuclear protein.  
SQ SEQUENCE 178 AA; 19157 MW; 832C61408C134DCF CRC64;  
Query Match 51.9%; Score 55; DB 2; Length 178;  
Best Local Similarity 55.6%; Pred. No. 4.1;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 CTKEGVLLKGGKREEKP 19  
|: ||| | ||| |||  
Db 4 CCEGVILTAKDKTEKP 21  
Search completed: December 29, 2005, 15:40:14  
Job time : 233 secs

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; OTHER INFORMATION: 2NIC1F (chimera 4)
US-09-709-188-26
Query Match      100.0%; Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
Db 261 LCTKEGVLLKGGKREKEKPF 280

RESULT 6
US-10-225-060-26
; Sequence 26, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: 2NIC1F (chimera 4)
US-10-225-060-26

Query Match      100.0%; Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
Db 261 LCTKEGVLLKGGKREKEKPF 280

RESULT 7
US-08-740-223A-14
; Sequence 14, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; TITLE OF INVENTION: Intercellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: mTL1
; LOCATION: 1..497
; OTHER INFORMATION: mouse TIR-2 ligand 1
US-08-740-223A-14

Query Match      100.0%; Score 106; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
Db 263 LCTKEGVLLKGGKREKEKPF 282

RESULT 8
US-09-709-188-14
; Sequence 14, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-709-188-14

Query Match      100.0%; Score 106; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREKEKPF 20
Db 263 LCTKEGVLLKGGKREKEKPF 282

RESULT 9
US-10-225-060-14
; Sequence 14, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; TITLE OF INVENTION: Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188

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;; PRIOR FILING DATE: 2000-11-09  
;; PRIOR APPLICATION NUMBER: 08/740,223  
;; PRIOR FILING DATE: 1996-10-25  
;; NUMBER OF SEQ ID NOS: 30  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 14  
;; LENGTH: 497  
;; TYPE: PRT  
;; ORGANISM: Mus sp.  
US-10-225-060-14

Query Match 100.0%; Score 106; DB 2; Length 497;  
Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKPF 20  
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DB 263 LCTKEGVLKGGKREKPF 282

RESULT 10  
US-08-373-579-2  
; Sequence 2, Application US/08373579  
; Patent No. 5650490  
; GENERAL INFORMATION:  
; APPLICANT: Davis, et al.  
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill River Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/373,579  
; FILING DATE: 17-JAN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/353,503  
; FILING DATE: 09-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/348,492  
; FILING DATE: 02-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,261  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/319,932  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cobert, Robert J.  
; REGISTRATION NUMBER: 36,108  
; REFERENCE/DOCKET NUMBER: REG 330-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 345-7400  
; TELEFAX: (914) 345-7721  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 498 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-373-579-2

Query Match 100.0%; Score 106; DB 1; Length 498;

Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LCTKEGVLKGGKREKPF 20  
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DB 264 LCTKEGVLKGGKREKPF 283

RESULT 11  
US-08-418-595-2  
; Sequence 2, Application US/08418595  
; Patent No. 5814464  
; GENERAL INFORMATION:  
; APPLICANT: Davis, et al.  
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill River Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/418,595  
; FILING DATE: 06-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,579  
; FILING DATE: 17-JAN-1995  
; APPLICATION NUMBER: US 08/353,503  
; FILING DATE: 09-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/348,492  
; FILING DATE: 02-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,261  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/319,932  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cobert, Robert J.  
; REGISTRATION NUMBER: 36,108  
; REFERENCE/DOCKET NUMBER: REG 330-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 345-7400  
; TELEFAX: (914) 345-7721  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 498 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-418-595-2

Query Match 100.0%; Score 106; DB 1; Length 498;  
Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKPF 20  
|||  
DB 264 LCTKEGVLKGGKREKPF 283

RESULT 12  
US-08-665-926-2